Net Volume Adjustment Factor

Sampling Standards and Procedures

Prepared by
Ministry of Sustainable Resource Management
Resource Information Branch
for the Resources Information Standards Committee

Version 4.0

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Net Volume Adjustment Factor Sampling Standards and Procedures
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1. page 59	- **Section 6.1.4.2** insert below the heading: The following calculations match the ones described in the paper "How to determine a minimum variance weight estimator relationship for a ratio estimator" by Bill Warren. This paper is published in Appendix 1. -**Section 6.1.4.2 step 3**. contains a formula for the calculation of ResidualP, this formula should read: $ResidualP = e_i^2/(x_i)^P$ - **Section 6.1.4.2 step 3**. contains a formula for the calculation of Ppvalue, this formula should read: Ppvalue $= P*ln(x_i)$ -**Section 6.1.4.2 step 5** contains a formula for the calculation of Ave_ResidualP, this formula should read: $Ave\_ResidualP = \sum ResidualP/No\ of\ trees.$ -**Section 6.1.4.2 step 5** contains the formula for the calculation of LP, this formula should read: $LP = -1*no\ of\ trees * ln(Ave\_ResidualP) - \sum Ppvalue$
2. page 74	-**Section 10.3.4.2** should include the statement: A tree fails to meet the standard if the number of penalty point equals or exceeds 10.
3. page 79	- Appendix 1 should be appended to the end of the standards and procedures. The contents of Appendix 1 should contain the document "How to determine a minimum variance weight estimator relationship for a ratio estimator" by Bill Warren as follows: **How to determine a minimum variance weight relationship for a ratio estimator** By Bill Warren Prepared for The Terrestrial Information Branch --- Let ε_i be the residuals and suppose $\varepsilon_i \approx N(0, \alpha \cdot x_i^{\,p})$, where the x_i are the volumes. The likelihood then: $$L = \prod_{i=1}^{n} \frac{1}{(2\pi\alpha x_i^{\,p})^{1/2}} \cdot \exp\left[-\frac{1}{2\alpha}\left(\frac{\varepsilon_i^{\,2}}{x_i^{\,p}}\right)\right]$$ $$\ldots = \frac{1}{(2\pi\alpha)^{n/2}} \prod_{i=1}^{n} \frac{1}{x_i^{\,p/2}} \cdot \exp\left[-\frac{1}{2\alpha}\left(\frac{\varepsilon_i^{\,2}}{x_i^{\,p}}\right)\right]$$ $$Ln(L) = -\frac{n}{2}\ln(2\pi) - \frac{n}{2}\ln(\alpha) - \frac{p}{2}\sum \ln(x_i) - \frac{1}{2\alpha}\sum \frac{\varepsilon_i^{\,2}}{x_i^{\,p}}$$

Suppose that p is known, then.

$$\frac{\partial \ln(L)}{\partial \alpha} = -\frac{n}{2\alpha} + \frac{1}{2\alpha^2}\sum \frac{\varepsilon_i^{\,2}}{x_i^{\,p}}$$

Equate to 0 and solve for α, then

$$\hat{\alpha} = \frac{1}{n}\sum\left(\frac{\varepsilon_i^{\,2}}{x_i^{\,p}}\right)$$

Substitute in *ln(L)*

$$\ln(L_p) = -\frac{n}{2}\ln(2\pi) - \frac{n}{2}\ln(\hat{\alpha}) - \frac{p}{2}\sum \ln(x_i) - \frac{n}{2}$$

The constants $\frac{n}{2}\ln(2\pi)...and...\frac{n}{2}$ and the factor ½ can be ignored. Thus evaluate:

$$L_p^{\,*} = -n\ln(\hat{\alpha}) - p\sum \ln(x_i)$$

I created a small artificial data set with n=10. I generated uniform random variables – on a pocket calculator – and used a table of the cumulative normal distribution to obtain standard normal random variables which were then recalculated. '***p***' was taken as 1.0. The data were then:

x_i	1	2	3	4	5	6	7	8	9	10
e_i	-.0510	-.2249	-.0091	.4720	.1968	.0710	-.3228	.0707	.2010	-.2656

Then with selected values of '***p***', I estimated α and obtained $L_p^{\,*}$, thus:

p	-1	-0.5	0	0.25	0.5	0.75	1	1.5	2.0
$L_p^{\,*}$	26.954	28.33	29.188	29.414	29.493	29.419	29.186	28.219	27.332

I have not checked the calculations but, since the points seem to follow a smooth curve, they would appear to be correct.

The maximum of $L_p^{\,*}$ occurs at $p \approx 0.5$. This would be the maximum likelihood estimate of ***p***. However any value for ***p*** in the range of (-0.1 to 1.1), say, would seem to be reasonably consistent with the data. In this way, feasible ranges for ***p*** could be obtained for different data sets and their intersection, hopefully not empty could be taken as a universal value for ***p***.

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1.0 Introduction

1.1 The NVAF Process

The Net Volume Adjustment Factor (NVAF) is an integral part of the Vegetation Resources Inventory (VRI). The NVAF is one of the components that must be completed in order to provide VRI sample data that meets all of the Ministry of Sustainable Resource Management (MSRM) inventory standards.

The NVAF is an adjustment factor that is used during sample compilation to produce unbiased estimates of net merchantable tree volume. It works to adjust the combined estimates of gross volume produced by the taper equation and decay and waste losses estimated by the cruiser through the net factoring process. NVAF sampling involves detailed stem analysis of sample trees, calculation of actual net volume, and calculation of the ratio between actual net volume and estimated net volume (where estimate net volume is obtained from net factoring and taper equations).

The NVAF adjustment is needed for the following reasons:

1. The cruiser estimated net volumes are obtained when a cruiser applies standard rules to determine the percentage of sound wood in a tree after detecting physical indicators of decay on a tree. The process of applying the decay estimation rules is known as *net factoring*. If no decay indicators are detected, a tree is considered to be 100% sound. However, a tree may have decay even if there are no visible indicators, or a cruiser may miss the indicators. Therefore, net volume may be over-estimated.

2. The rules used to associate decay indicators with amount of decay are based on expert knowledge, and past experience. As would be expected, the rules may over-estimate or under-estimate the amount of decay on the average for a ground sample project. For more information on how the rules are applied, please refer to the *Vegetation Resources Inventory Ground Sampling Procedures* manual (available on the websitehttp://srmwww.gov.bc.ca/tib/vri/vri/standards/index.html#vri).

3. The BEC-based tree taper equations may over-estimate or under-estimate whole stem volume when applied to local areas.

1.2 Principles of the NVAF process

The NVAF influences the VRI net volume, in that it is applied as an adjustment. The principles of the VRI sample data collection require that the results be unbiased. For this reason, it is required that the following principles be followed during NVAF data collection:

1. The sample polygons and tree selection should allow for all elements in the target population to have a fair chance of being included in the sample.

2. Valid NVAF data will be collected according to standards specified by the MSRM.

3. The computed NVAF(s) will be used to adjust the VRI net volumes for the relevant inventory project during data compilation.

4. The cruiser and stem analysis data will be provided to MSRM for building an unbiased provincial volume and decay database.

Overview of NVAF Data Collection and Analysis Steps

The NVAF data collection occurs in two sequential steps, with each step requiring a separate visit to the field. These data collection steps are:

Step One

The first step of NVAF data collection involves selection of sample trees from a large number of standing trees chosen by the cruiser. It consists of 5 stages:

1. Selection of polygons.

2. Selection of points within the sample polygons where a VRI 5-plot cluster will be established.

3. Identification trees within the auxiliary plots which will be eligible for consideration in the creation of a tree list from which to select sample trees to be felled.

4. Collection of preliminary measurements, which include net factoring to facilitate the estimation of tree net volume.

5. Selection of NVAF trees to be felled from the tree list by stratum or subpopulation. The number of sample polygons and sample trees is normally documented as part of a VRI sample plan.

Step one is described in detail in sections 2, 3 and 4 of this manual.

Step Two

The second step of NVAF data collection involves accurate measurement of actual net volume on the ground through stem analysis. The sample trees selected in Step 1 are felled and sectioned to measure actual net volume. Step two is described in detail in section 5.

This two-step NVAF data collection process sometimes limits the timing of the NVAF results. While the VRI data collection may be completed in one year, the NVAF data collection may require two or more years. (More efficient data collection methods that will allow for an improvement in scheduling are under investigation.)

The NVAF data analysis involves compiling both the cruiser's estimates of net tree volume and actual net tree volume obtained from the felled trees. It also involves calculating the selection weights of each tree. These data are then used to compute the NVAF(s) for a project by sub-population, or by strata. The NVAF is computed as the ratio of ground volume to cruiser volume. Typically, the NVAF is computed as:

$$NVAF = \frac{\text{weighted actual net volume per tree}}{\text{weighted cruiser estimated net volume per tree}}$$

where: *NVAF* = the ratio used to adjust VRI net volumes during compilation

Actual tree volume = amount of sound wood fibre tree-volume measured on the ground, through stem analysis, determined to be free of decay and waste.

Cruiser estimated volume = estimated amount of wood fibre volume, determined through the application of net factoring rules, and assumed to be free of decay and waste.

All volumes describe the portion of the stem defined as "close utilization", that is the wood between a 30 cm stump and a 10 or 15 cm top diameter.

The NVAF is then used to adjust compiled net volume estimates made by cruisers in an inventory project. The NVAF data analysis is described further in sections 6 and 7.

A diagrammatic representation of the VRI net factoring, stem analysis and NVAF processes is shown in figures 1-1 and 1-2.

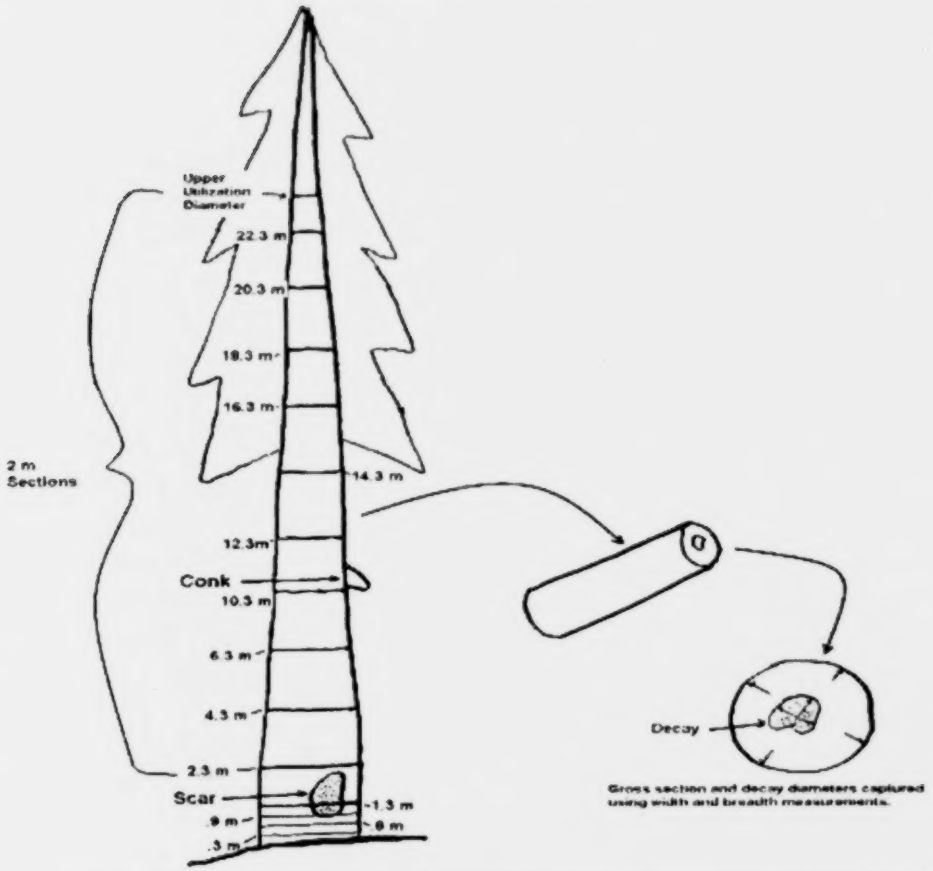
Summary of Loss Factors Process	
Risk Group	Risk Group Rule
3	Presence of conk places the tree into risk group 3.

Summary of Net Factoring Process

Log Length	Grade	Net Factor
15m	X	100%
Net Factor Rule: No visible decay.		
10m	Y	50%
Net Factor Rule: Conk rule: 4m above and 6m below at 50% sound wood.		
3m	X	91%
Net Factor Rule: Log volume estimated at .35m^3, scar void volume estimated at 0.03m^3.		
Net Factor = (.35-.03)/.35		

Log Length	Grade	Net Factor (% Decay)	% Waste	Gross Close U Volume (m^3)	Net Close U Volume (m^3)
15	X	100	0	.2	.2
10	Y	50	0	.7	.35
3	X	91	0	.31	.28
Total Tree Volume by VRI Net Factoring Process				1.21	.83
Total Tree Volume by Loss Factor Process		29.7	12.4	1.21	.7

Figure 1-1. Comparison Between Two Tree Net Close Utilization Volume Estimating Processes – Loss Factors vs. Net Factoring



Actual Tree Volumes and Percent Loss			
% Decay	% Waste	Gross Close U Volume (m^3)	Net Close U Volume (m^3)
27.8	5.6	1.13	0.75
VRI Estimate of Tree Volumes and Loss			
31.4	0	1.21	0.83
NVAF Ratio (Actual / Estimate)			0.90

Figure 1-2. NVAF Stem Analysis Diagram

1.3 Purpose of the Manual

The purpose of this manual is to provide inventory managers and technicians with instructions regarding sample selection, data collection and data analysis required to compute unbiased NVAF values for a VRI project.

This manual also discusses potential problems and issues that may arise in the various components of the NVAF process.

1.4 Components of the Manual

This manual consists of 10 sections. A brief description of the contents of each section is provided here for quick reference.

Section 1: Provides the broad highlights of the manual.

Section 2. Describes the process used to determine number of polygons to be visited for the collection of NVAF data. It also describes how the polygons should be selected.

Section 3. Describes the procedure for identifying locations and number of plots to be visited in the NVAF sample polygon. These locations provide the pool of trees from which a sample of trees is selected for stem analysis.

Section 4. Describes the procedure for selecting trees to be felled.

Section 5. Describes the stem analysis process.

Section 6. Outlines the data editing processing and analysis.

Section 7. Outlines the potential issues that may arise during data analysis.

Section 8. The NVAF data is valuable for purposes other than adjusting VRI net volume. It will also be used to build a more modern volume and decay database. This section outlines the data requirements and how it will be stored.

Section 9. The NVAF adjustment in the compiler may be unclear to many inventory users. This section contains a brief description of how the adjustment is applied.

Section 10. The complexity of the NVAF data collection requires that rigorous quality assurance be implemented. This section provides the quality assurance procedures and standards.

Section 11. Defines key terms to ensure that the user has a quick reference in case they encounter terms or acronyms with which they are not familiar.

1.5 Roles and Responsibilities

Generally, this manual is written to facilitate independent use without close guidance from MSRM staff. Inventory managers or technicians should be able to follow the steps in the manual to achieve their objectives.

Headquarters staff will track ongoing NVAF projects, and may participate in training, mentoring and quality assurance, if resources are available to do so.

The Data Service Center staff will coordinate communication between headquarters and proponents implementing NVAF projects.

Proponents implement NVAF projects will conduct sample selection, organize fieldwork and process field data. They will communicate arising issues to Data Service Centers who in turn will pass it on to headquarters staff.

2.0 Selection of Polygons

Selection of sample polygons involves several steps:

1. Constructing a sampling frame
2. Stratifying the sampling frame
3. Determining the number of sample polygons
4. Selecting sample polygons

Each of these steps is described in detail below.

2.1 Constructing a Sampling Polygon Frame

Generally all polygons in an inventory unit (or project) should be eligible for inclusion in the NVAF sample. The polygon selection can be achieved through various options which include:

- Selection of polygons directly from the polygon list
- Sub-selection of polygons from the list of polygons selected for VRI ground sampling

In either case, the polygons are selected with probability proportional to polygon size. In the majority of the cases, the NVAF sample polygons are sub-selected from the VRI sample for the following reasons:

- The NVAF sample locations are also included in the overall compilation for the VRI sample.

- The VRI sample is a random representation of the population in a target inventory unit; therefore, a sub-selection from the VRI sample polygons will also be a random representation of the same population.

- The VRI adjustment is applied to the VRI ground sample compilation, but can technically be applied to any other VRI-type data collection in the inventory unit in the future if the same net volume deduction rules are used.

- Sub-selection of NVAF sample polygons from the VRI list simplifies the NVAF sample selection process.

To construct the sampling frame for NVAF, obtain all the polygonal attribute data for the VRI sample polygons. Essentially, a list of such polygons and the associated attributes constitutes the polygon sampling frame for NVAF.

The VRI sample polygons are selected with probability proportional to size with replacement (PPSWR). In the absence of a VRI list of sample polygons, the NVAF sample polygons should be selected directly from the population list of all polygons in the inventory unit using PPSWR. A detailed description of the PPSWR sample selection process is provided in the *Vegetation Resources Inventory Sample selection Procedures for Ground Sampling* manual (available on the website http://srmwww.gov.bc.ca/tib/vri/vri/standards/index.html#vri).

2.2 Potential NVAF Sample Selection Scenarios

The following scenarios may arise during the NVAF sample selection process:

1. VRI ground data collection occurs prior to NVAF sample selection. In this case the sampling frame is clearly defined, and NVAF sample polygon selection occurs with no problems.
2. NVAF sample selection occurs prior to VRI ground data collection. Some issues may arise due to inaccessible and unsafe samples, samples with prohibitions on felling and to shortfalls in some types (usually species) of sample trees.
3. NVAF sample selection requires additional polygon selection in addition to existing VRI sample polygons. This occurs if a stratum identified for NVAF is under-represented in the VRI sample, but because of its unique net volume characteristics, it requires an augmented sample to confirm potential hidden decay or taper error issue. For instance, a species of significant interest may not be adequately covered by the VRI sample polygons. In such cases, a stratum with polygons that may contain the species of interest may be extracted from the population, and a sample is then selected from the stratum using PPSWR.

NVAF sample selection occurs in the absence of any VRI sample polygons. In this case a list of all polygons in the target population is compiled and PPSWR is applied to select the NVAF sample polygons.

2.3 Stratification of Polygons

The VRI sample polygons may be pre-stratified by inventory attributes such as age (Mature/ Immature) or by leading species. This applies when the NVAF data collection is conducted prior to ground data collection. If ground data is available, the VRI sample polygons may be stratified by ground measured site height and leading species.

The use of ground data in the stratification is a refinement, in that it eliminates potential miss-classification error that may occur in the inventory data. But in the absence of ground data, the inventory data will suffice.

2.4 Determining the Number of Sample Polygons

The number of polygons to be included in the NVAF is often determined to achieve cost efficiency since the NVAF ground data collection exercise is quite costly. It is estimated that the cost to collect data from a single destructive sample tree, varies from $300 to $1000. Most of the high expense is due to travel to a sample polygon. For this reason, it is more cost effective to have a few sample polygons where many trees are selected for felling rather than have many polygons where one or only a few trees are felled.

In most NVAF projects, the number of sample polygons is estimated based on the target number of trees desired for a given project. It is essentially an approximation exercise as follows:

1. The number of trees required to meet an NVAF sampling error requirement for an inventory unit or sub-unit is determined. (This will be described further in section 4). Let's say, the require number of trees to be destructively sampled is 60. This is the number of trees that will be felled and stem analysed to generate NVAF data.

2. Based on past experience, the general guideline for the determination of the number of ground samples is to select one ground sample for every 3 sample trees.
3. The number of sample polygons is then computed by dividing the number of estimated sample trees (60) by the number of trees (3) we expect to obtain from an average sample polygon. The outcome in this case is 20 (i.e., 60/3=20).
4. The estimation process provided above is for illustration only. The more important sample size determination is that of the number of trees required to meet a predetermined sampling error. This will be discussed in more detail in section 4.

2.5 Polygon Selection

In the description below, is assumed that the NVAF sample polygon selection occurs after the first selection of VRI polygons.

The NVAF polygon selection from the list of VRI polygons is, in most cases, by systematic selection with a random start. The polygons may be sorted by leading species or other criteria of interest. A systematic selection minimizes the lack of representation that is common to small random samples. A sort by leading species can ensure that there are sufficient numbers of trees tallied by the common tree species in the NVAF ground samples. The following procedure is followed:

1. Using the NVAF polygon sample size, determine a selection interval "k". This computed as the number of VRI samples "n" divided by the NVAF sample size m, i.e., (k=n/m). k should be rounded to produce an integer value.
2. Select a random number between 1 and "k". This number identifies the first polygon to be selected. For instance if the random number is 3, then the 3rd polygon in the list is selected.
3. Add the interval k to the random number. This sum identifies the second polygon to be selected.
4. Repeat step 3 until the required number of polygons is obtained.

This selection process produces a list of NVAF sample polygons which have selection probabilities proportional to polygon area, because the VRI sample is selected with PPSWR.

The selection of polygons from the VRI sample polygons list may also be based on simple random sampling. In this case, the VRI list of sample polygons, are each assigned a random number, and then the list is sorted by random number. The first *m* polygons that appear in the randomized VRI list are the NVAF sample polygons, *m* is the polygon sample size for NVAF.

After the first selection of NVAF sample polygons, it may be determined that one or more species with a decay interest was overlooked or under-represented. The VRI polygons that are not in the NVAF list may be screened to extract additional polygons, which were not included during the first sweep. This rarely occurs when the VRI polygons are pre-stratified, and NVAF samples are selected by strata.

The sample selection process within a stratum is essentially the same as with the un-stratified VRI polygons. The selection is random.

When stratification occurs, independent NVAF estimates and statistics are expected for each stratum. Thus a sample size is determined for each stratum depending on availability of resources (funding) and business needs. Generally, the number of sample polygons for each

stratum may vary from 5 to 20 polygons, depending on the number of trees required in a stratum.

2.6 Procedure for Replacing Inaccessible and Unsuitable Polygons

There are two scenarios, which may require the replacement of a selected NVAF polygon, and they are

1. A selected polygon is found to lie in an area that is outside the population of interest. This scenario includes NVAF sample polygons that are found to have no trees larger than 12.5 cm in dbh.
    - For this scenario a replacement sample should be selected randomly from the VRI ground sample.
2. A selected polygon is found to be inaccessible by all reasonable means of access. This scenario includes polygons that are in the target population. But where destructive sampling is prohibited.
    - For this scenario, a matching process based on principles outlined in the Inaccessible Sample Locations Procedures manual should be used to find a VRI ground sample location that matches the description of the inaccessible location.

Sample polygons should not be replaced for reasons other than those outlined above. To do so would create a bias in the resulting NVAF. Ad hoc substitutions of samples undermine the integrity of the NVAF data.

3.0 Sampling and Enhancement of NVAF Polygons

The purpose of sampling and enhancement of the NVAF polygons is to tally a large set of trees and to collect a set of attributes for the tallied trees, known as enhancement, from the population of interest and to estimate whole stem gross and net volume on a subset of those trees. Enhancement means taking additional measurements beyond those normally done for trees in the auxiliary plots of VRI project. Sampling and enhancement for NVAF involves:

1. Establishing the VRI clusters
2. Selection of plots within VRI clusters to enhance
3. Estimation of tree attributes
4. Estimation of cruiser net volume.

3.1 The VRI Cluster Establishment

Within each NVAF sample polygon a random point is selected. A more detailed description of the selection of a random point within a sample polygon is provided in the *Vegetation Resources Inventory Sample Selection Procedures for Ground Sampling* manual (available on the websitehttp://srmwww.gov.bc.ca/tib/vri/vri/standards/index.html#vri). At the random point location, a five-plot cluster is established (see Figure 3-1). The IPC is located exactly at the location of the selected random point. Once the IPC is located, the measurement of the trees at the IPC, and the auxiliary plots begins.

The VRI 5-plot cluster that has been alluded to earlier is oriented as illustrated below:

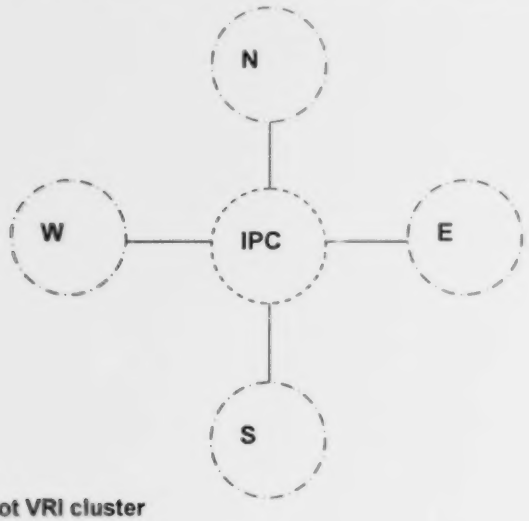


Figure 3-1. Five-plot VRI cluster

The north (N), east (E), south (S) and west (W) auxiliary plots are typically located 50 meters from the integrated plot center (IPC). For the conventional VRI, detailed tree attribute data (i.e., tree heights, diameter at breast height (dbh), and pathological indicators of decay, height to crown, tree form, etc.) are collected at the IPC. For live trees in the auxiliary plots, except

in cases where some trees are enhanced, only tree species and dbh are collected. Dead trees are normally not tallied so enhancement for NVAF purposes includes a sweep for dead trees in addition to collection of attributes. Further details of VRI ground sampling are available in the *Vegetation Resources Inventory Ground Sampling Procedures* manual (available on the website http://srmwww.gov.bc.ca/tib/vri/vri/standards/index.html#vri

3.2 Determination of Plots Within Cluster to Enhance

NVAF enhancements are done only on the auxiliary plots of the VRI ground sample. This allows the trees and other vegetation on the IPC plot to be available for future measurements.

In the conventional VRI, up to four auxiliary plots are placed at cardinal directions around the IPC plot and all of the auxiliary plots of a sample selected for NVAF are enhanced.

3.3 Variation From 4-Plot Enhancement

Some variations to the conventional practice of the enhancement of all of the auxiliary plots of the NVAF ground sample have been tested in order to gain additional efficiencies from the sample.

There are some situations where a proponent may elect to enhance a subset of auxiliary plots of a NVAF ground sample instead of the full complement of four plots. The situations that may lead to a selection of a subset of plots can arise in complex stands of old trees where the NVAF enhancements are difficult and may require a return visit to the sample to complete the work. In the interest of sampling efficiencies, a number of proponents have successfully implemented this approach through the unbiased selection of two auxiliary plots in each NVAF ground sample. However, in order to obtain an adequate sized tally of some of the less common tree species, it may be necessary to increase the ground sample size. In most cases this will not be a problem but may occur in units that intend on sampling a stratum of important but uncommon tree species. Examples include a yellow cedar stratum, or a mature Douglas-fir stratum on the coast.

In another pilot, one auxiliary plot was selected for enhancement and all trees in the selected plot were felled for NVAF stem analysis. This approach does not work well if the species tree distribution is clumped with in a polygon. In addition, the target auxiliary plot has to be selected prior to the field work. Consequently, it is difficult to predetermine the number of trees that will be felled, prior to the completion of the field data collection. In one extreme, the selected auxiliary plots may fall on areas within a polygon where there are few or no trees. This may require the selection of additional plots if the first pass does not produce enough trees.

In another extreme, the selected auxiliary plots may fall on parts of the sample polygons with a large number of trees. It may require a modification of the tree selection procedure to allow the exclusion of some trees in order to meet the project objectives within budget. This pilot produced a reasonable number of trees, but the approach was abandoned because of the uncertainty associated with its implementation.

3.4 List of Key Attributes Recorded

The key standard VRI attributes required for this purpose are:

Tally of dead trees

Tree species

Height

Diameter at breast height

Location of loss indicators of presence of wood decay

Log lengths

Estimates of percent sound wood less decay (net factor) for each log

Live/dead status of the tree

Log grades

These data should be collected to the VRI standard for the NVAF sample polygons in the IPC plot.

A key non standard VRI attribute to collect is comments about individual trees on their extreme unsuitability as NVAF sample trees which would include the following:

- Major wildlife use, which includes eagle nests, bear dens and the like
- Unsafe tree conditions that would imperil the faller
- Site conditions that would prevent the tree once felled from being sampled, which include trees above bluffs and waterways.

3.5 List of Other Attributes Recorded

Additional site and stand conditions, collected by the cruiser, can facilitate the work of the destructive sampling crew. Useful information includes description of the conditions of the:

- Falling difficulty
- Sample access
- Terrain
- Brush
- Windfall and slash

3.6 Timing of NVAF Enhancements

There is some flexibility around the timing of the NVAF enhancements and the options available to a proponent are dependent on the status of their VRI ground sampling and the availability of funding and qualified personal. There is one immutable fact to NVAF and that is the NVAF sample trees must be selected from a list of previously tallied trees.

Enhancement at the Time of Ground Sample Establishment

This appears to the most efficient method since the sampling crew is on site and usually has sufficient time to complete the establishment and enhancements in one field day. If the stand conditions in the sample are predicted to be too complex to complete the enhancements within the day, an unbiased selection of a subset of auxiliary plots is recommended.

Enhancement After Ground Sample Establishment and Before Destructive Sampling

This option is useful for proponents that have completed their ground sampling and must go back in to complete their NVAF sample. Efficiencies are gained through the provision of sample tree details for the subsequent destructive sample operation and through the identification (and replacement) of unsafe or inaccessible samples.

Enhancement at Time of the Destructive Sample

This option is useful for proponents that have completed their ground sampling and must go back in to complete their NVAF sample. Unsafe or inaccessible samples can be identified and replaced. Live trees can be selected using the attributes (species, dbh) collected in regular ground samples. Tree enhancements can be done immediately prior to the tree felling. However, inefficiencies arise in the lack of tree details for the destructive sampling operation and in the selection of dead trees (which are not tallied in regular ground sample auxiliary plots). The dead tree selection process to use in this situation is described in Section 4.5

3.7 Estimation of Net Volume by Cruiser

Net tree volumes are compiled by the VRI tree compiler using the cruiser's estimates of sound wood volume. Volumes are compiled net waste and decay excluding the stump and top (close utilization). See Section 6 on the compilation of predicted or estimated tree volumes.

4.0 Selection of Trees to Fell

Recall that the first step of the NVAF process involves several stages including sample polygon selection, establishment of VRI ground sample clusters, enhancement of the auxiliary plots, and sample tree selection. The sample tree selection involves assembling a tree list from the enhanced auxiliary plots by sub-population or strata, and selecting a sample of trees for felling from it. The following sections outline the sample tree selection components that include:

1. Constructing a tree sampling frame
2. Stratifying the tree population
3. Selecting the sample trees to be felled.

4.1 Tree Sampling Frame

The tree records and data from the NVAF polygons are used to construct the sampling frame for the selection of trees to be felled for stem analysis. A tree list from the NVAF polygons, and the attributes in the tree list, constitute the tree sampling frame.

In addition to the tree attribute listed in the sub section on "List of attributes recorded", information on location and navigation to the NVAF plot clusters should also be provided. The information should include:

- Cruiser's notes on access and navigation to NVAF plots.
- Maps and photos identifying the geographic location of plots.
- Map number and sample polygon number.
- Cluster identification number.
- Plot identification symbols or numbers.
- Tree identification numbers.

These data are necessary for relocating the NVAF plot clusters, for the purposes of conducting the second step of the NVAF data collection.

Documents, records, the sampling frame, and sampling weights should be archived for reference during data analysis. A more detailed explanation of weight computation and other attributes is provided in the data analysis section.

4.2 Stratification of Trees

The tree list created from the NVAF polygons can be post-stratified based on, for example, dbh and tree species (see Table 4-1 below) to examine the sample tree distribution. The entries in this table are the number of trees tallied by species and dbh. Dead trees are treated separately from live trees.

Table 4-1. A Summary Table Showing the Number of Trees Tallied by Species and dbh Class After Enhancement of NVAF Polygons

Dbh Class	Species		
	Fd	Pl	Other
12	0	10	0
14	5	15	0
16	6	8	2
18	4	6	3
20	8	8	7
22	10	4	1
24	11	2	3
26	2	3	0
28	4	1	2
30	1	5	4
32	3	2	2
34	5	3	1
>34	3	4	0
Total	63	71	25

Other summary tables may be generated from the tree list. Table 4-2 shows the relative distribution by species and age. The coordinator of an NVAF project may summarise the tree list data by any categories that might meet local business needs.

Table 4-2. An Example of Summary data From the Enhanced NVAF Polygons

Species	Mature stratum		
	Relative size in population (vol)[1]	Number of trees tallied	Proportion of trees in sample[2]
Fd	60%	63	35%
Pl	28%	71	40%
Other	12%	45	25%
Total	100%	179	100%

These tables can be produced by stratum, or for all strata combined. Individual strata tables are more useful as they assist in the detection of tree distribution deficiencies and adjustment sample allocation if necessary. If major tree distribution deficiencies are detected, it may be necessary to go back to the field to enhance more trees to add to the tree list.

4.3 Tree Selection Process

The tables described in the section above define the sub-populations or strata from which samples are selected. Sample selection is separate for each sub-population or stratum, and for live and dead trees. Dead trees are typically put in a single stratum.

The sample tree selection process involves determining the overall sample size (the number of live and dead trees to fell), allocating the overall sample to sub-populations or strata, and then selecting sample trees within the subpopulations or strata.

4.3.1 Sample Size Determination

The formal process for determining sample size (live trees) for an NVAF project is to target a sampling error E for the overall NVAF, estimate the population coefficient of variation (CV) of the NVAF, and then determine the approximate sample size using the following formula:

$$n = [\frac{t * CV_{sample}}{E}]^2$$

where t is the "t-value" associated with a given probability and degrees of freedom.

CV_{sample} is an estimate of the population CV from neighbouring or related NVAF projects.

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[1] This information is obtained from inventory records prior to NVAF ground data collection.

[2] This proportion is computed from number of trees, but it can be based on tree volume or other convenient factor.

For example, if the estimated CV of the NVAF is 35%, and the target sampling error E is 10% (95% probability), then the overall sample size would be about 50.

The sample size for live trees calculations suggested here are general guidelines, not exact requirements. The sample size used in practice is usually a trade-off between the calculated sample size and the expected cost, timing, and credibility of the NVAF. The calculated sample size may be increased arbitrarily to allow for post-stratification, and to meet local business needs. Experience from past NVAF projects suggests that an overall sampling error of approximately 10% (95% probability) is usually obtained with a sample size of about 50 live trees for all strata combined.

The sample size for dead trees is typically low (5-10) and is set arbitrarily, primarily considering cost; stem analysis is more time consuming on dead trees than on live trees. As well, net dead volume is not of significant importance in most management units.

4.3.2. Sample Allocation

The process of determining the number of live or dead trees to select for a sub-population or stratum within an inventory unit is subjective. It is based on several factors including past experience, expert knowledge of variation within a given sub-population or stratum, cost of sampling in the stratum, and the relative importance of the various strata.

For the mature and immature sub-populations, less variation around the ratio of actual volume over the estimate of volume is expected in the immature component. The immature trees are relatively free of defect and have a regular stem form

The trees in the mature sub-population however have more variation around the ratio of actual to estimate of volume due to their irregular stem form and higher incidence of decay. Consequently, the mature sub-population is typically allocated more samples than the immature.

For the species strata, sample size determination depends on four factors, which are:

- Significance of the species in determining total inventory volume for an inventory unit.
- The variability around the ratio of actual over the estimate of volume of the species.
- The desired level of sampling error for the species
- Availability of funds to complete the project.

Past experience indicates that fairly reasonable sampling errors (< 15%, at 95% probability) of the NVAF can be obtained with sample sizes ranging from 20 to 30 for a stratum.

Table 4-3 shows an example of how samples may be allocated to mature and immature sub-populations and species strata with in the mature sub-population.

Table 4-3. Example of Sample Allocation by Sub-population and Strata

	Immature	Mature			
	All Species	Fd	Pl	Other	Total
Allocation (number of sample trees)	20	20	30	30	100

4.3.3 Tree Selection

The following sorted list procedure should be used in selecting trees within a sub-population or stratum (Tables 4-4 and 4-5):

- create a matrix of sub-populations and strata as may be desired to meet business needs
- generate a tree list for each sub-population and stratum using the first step NVAF tree data.
- Sort the tree list by dbh - an even distribution by dbh is desired. An even distribution may be obtained without this step, but sorting provides some assurance of it.
- Divide the number of trees in the stratum (N_j) by the desired sample size (n_j) to obtain a selection interval, k. This number should be rounded to produce an integer.
- Generate a random number between 1 and k. The random number identifies the first random tree in the tree list.
- Add k to the random number to select the second tree. The sum of the random number and k is an accumulated selection number.
- Add k to the accumulated selection number select the third tree, and repeat the process until n_j trees are selected.

Table 4-4. A Summary Table Showing the Number of Tallied Trees, Number of Sample Trees, the Selection Interval (k) and the Random Start Number for Species and Maturity Strata

	# Trees Tallied (N_j)	# of Sample Trees Allocated (n_j)	k Value	Random Number
Fd	63	20	3	3
Pl	71	30	2	1
Other	45	15	3	2
Mature Total	**179**	**65**		
Immature	120[3]	15	8	5
Overall Total	**299**	**80**		

[3] The number of immature trees tallied is not provided in Table 4-3.

Table 4-5 provides an example of a tree list. The n_j trees selected from such a list constitute the list of trees that will be felled and sectioned for stem analysis.

The trees can also be selected randomly instead of systematically as previously described. This random selection can be achieved by generating n_j random numbers between 1 and N_j for each stratum j. When a random number identical to a sequence number for a tree, the tree is selected.

Table 4-5. An Example of the Selection From a Tree List

Sel_#	Tree Strata	Map#	VRI Samp #	Poly#	Clst_ id	Plot#	Tree#	Tree attributes			...	Vol
								Dbh	Ht	L/ D		
	Fd										...	
	Fd										...	
1	Fd										...	
	Fd										...	
	Fd										...	
2	Fd										...	
	Fd										...	
	Fd										...	
3	Fd										...	
	Fd										...	
	Fd										...	
4	Fd										...	
	Fd										...	
1	Pl										...	
	Pl										...	
2	Pl										...	
	Pl										...	
3	Pl										...	

Sel_#	Tree Strata	Map#	VRI Samp #	Poly#	Clst_ id	Plot#	Tree#	Tree attributes			...	Vol
								Dbh	Ht	L/ D		
	PI										...	
4	PI										...	
	PI										...	
5	PI										...	
	PI										...	
6	PI										...	
	PI										...	
7	PI										...	
	PI										...	
8	PI										...	
	PI										...	
9	PI										...	
	PI										...	
10	PI										...	
	PI										...	
11	PI										...	
	PI										...	
	PI										...	
12	PI										...	
	PI										...	
13	PI										...	
	Other										...	
1	Othe r											

	Other											
	Other											
2	Other											
	Other											
	Immat											
	Immat											
	Immat											
	Immat											
1	Immat											
	Immat											
	Immat											
	Immat											
2												
	Immat											
	Immat											

- The selected trees are identifiable by map number, sample number, cluster identification, plot number and tree number based on tagging from the first step of the NVAF sample selection. Consequently, it is reasonably easy to relocate the trees in the field when the Step two of the NVAF data collection.

4.4 Sample Tree Replacement

All selected trees should be used in the computation of the NVAF. However, there are a number of situations where one or more selected NVAF trees may need to be replaced. These situations include:

- A selected tree is unsafe to fall.
- A selected tree is situated in such a way that if felled, it would be impossible to measure, i.e. the tree is above a bluff or a waterway.
- A selected tree is found to be an active wildlife tree or has other very special characteristics that would outweigh its importance to the NVAF sample.
- A catastrophic natural occurrence damages a selected tree prior to stem analysis to the extent that the volume of the damaged tree does not relate to the tree at the time of enhancement.

If this occurs, then select a replacement tree through a random selection of a tree with a similar dbh from the group or stratum where the tree be longed. It is essential to select the replacement trees without bias.

There is some flexibility in the replacement process as per:

1. Select the replacement tree from the polygon where the loss occurred by selecting a replacement tree from other auxiliary plots of the cluster, or if none are available, selection of tree along a random bearing from the cluster, or
2. Select the replacement tree from the list of tallied trees.

4.5 Dead Tree Selection if Not Previously Tallied

If enhancements are being done concurrent with the destructive sampling, then all dead trees within the selected auxiliary plot must be tallied and enhanced prior to selection. Once the subset of dead potential trees is identified, the sample tree can be selected without bias. Steps to take for the selection process are:

1. Randomly select an auxiliary plot from each of the NVAF ground samples
2. Once at the selected auxiliary plot, tally all dead trees
3. Estimate the subset of dead potential trees through an estimate of % sound of each dead tree. Trees that are obviously under 50% sound wood can be ignored. Trees that are borderline 50% sound should be properly net factored.
4. Use the following formula to determine the trees that are actually dead potential:

$$Tree\_\%sound\_wood = \frac{\sum(\log\_length * \log\_\%\_sound)}{\sum(\log\_length)}$$

   Any tree that is more than or equal to 50% sound wood can be considered to be dead potential.

5. Use the random number table to select one tree for destructive sampling.
6. Enhance the selected dead sample trees using the regular enhancement process.

5.0 Stem Analysis Data Collection

5.1 Introduction

This section outlines the tasks required to collect stem analysis data on selected trees. The standards and procedures for the NVAF stem analysis sampling adhere to those for volume and decay sampling.

5.1.1 Data Collection Software

NVAF data must be captured in the field using the DVHand and Host data collection software.

5.1.2 Principles

NVAF sampling entails the collection of data that will allow for the calculation of actual net and merchantable tree volume. Log sections are kept short at a 2 m length to minimize errors around the formula, Smalians, used to calculate log volume. The cross sectional area of decay and other losses to sound wood in each section are precisely determined and exclude any contiguous areas of sound wood.

5.1.3 Timing of Sampling

NVAF sampling should only be conducted when the wood is not frozen. This is due to the difficulty in determining decay in frozen wood.

5.2 Supplies and Materials

Table 5-1. Materials required for stem analysis.

• map and photo holder	• compass
• field notes for sample	• clinometer
• NVAF Standards and Procedures manual	• 30 or 50 m (Eslon style) tape
• user guide for data collection software (DVHand)	• diameter tape
• handheld computer	• thin pointed knife $\geq$ 10 cm blade
• spare batteries for the handheld computer	• axe $\geq$ 2.5 lb
• regional biogeoclimatic ecological classification (BEC) book	• indelible felt markers or log crayons
• VHF radio or satellite phone	• 15 cm scale ruler starting at 0 cm
• first aid/survival gear	• metric carpenter's tape
• field book with blank field sheets	• spray paint
• pencil	• flagging tape
• calculator	• high powered hand lens

- altimeter or topo map
- site index age correction tables

5.3 General Procedures

The general procedures for the stem analysis are outlined sequentially. The detailed procedures follow further in the section.

1. **Describe Field Orientation and Navigation**

   - Access the sample.
   - Identify the sample.
   - Identify the plot.
   - Identify the tree.

2. **Record Sample and Plot Attributes**

   - Record sample attributes.
   - Record plot attributes.

3. **Assess Tree(s) for Path Indicators**

4. **Mark and Measure Standing Trees**

   - Limb branches and remove obstructions.
   - Relocate and mark the high side of the tree.
   - Mark the butt taper heights.
   - Measure the butt taper diameter outside bark (DOB).
   - Cut bark windows and measure double bark thickness (DBT).

5. **Fall, Buck, and Measure Age of Trees**

   - Fall and limb the tree.
   - Buck out the 1.3 m cookie.
   - Buck out the 0.3 cookie.
   - Count age.

6. **Mark and Measure Felled Tree**

   - Reconstruct the tree if broken during falling.
   - Run measuring tape along stem of tree.
   - Locate crown height.
   - Identify primary and secondary leader(s).
   - Locate heights of primary and secondary leaders.
   - Locate the upper utilization diameter inside bark heights of primary and secondary leaders.
   - Locate, mark, and measure broken top(s), fork(s), and crook(s).
   - Identify and measure path indicators.
   - Mark significant taper changes.
   - Mark off sections above 1.3 m and between the Utop.
   - Assign leader number(s) to secondary leaders.
   - Buck sections.
   - Buck "cookies".

- Measure DIB of each section.
- Identify decay characteristics and shape.
- Identify decay by section.
- Measure decay.
- Measure voids.
- Determine length of decay by section (intermediate bucking).
- Check path indicators for hidden decay.
- Cut blaze on tree stump and identify sample tree.

7. **Data Edits and Processing**

- Deletion of unwanted trees.
- Ensure consistency of broken top attributes.
- Ensure all decay length information is entered.
- Ensure decay attributes are entered.

5.4 Detailed Procedures

5.4.1. Describe Field Orientation and Navigation

5.4.1.1. Access the Sample

Use the existing sample field documentation to determine the location of the sample and determine the nearest access point. Minimize the travel distances and time to the sample. For helicopter access, the UTM coordinates of the tie point and IPC must be used. If the original helispot is far from the sample, create a closer one if possible. Crews must have alternative samples as a contingency.

5.4.1.2 Identify the Sample

The sample identity consists of region, compartment, and VRI ground sample number. The region and compartment information can be obtained from the inventory database, forest cover maps or from the MSRM Victoria office.

5.4.1.3. Identify the Plot

The plot is identified by its cardinal direction from the IPC. The following numbers differentiate the plots:

1 = north plot

2 = east plot

3 = south plot

4 = west plot

5.4.1.4. Identify the Tree

The tree is identified with the same tree number given in the VRI ground sampling phase. Clearly identify the sample tree by blazing the stump and recording:

- project code
- sample ID
- plot ID

- date
- initials of crew members

For example, if the sample tree is #5 on the south plot of sample 51 of the TFL 55 VRI, then record the following: **TFL 99 Sample 51 tree S-5 sampling crew initials, date** (Figure 5-1)

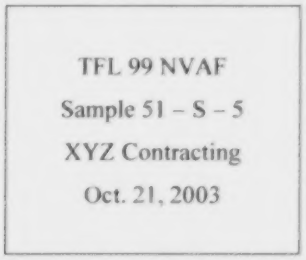


Figure 5-1. Tree Identification.

To mark the tree, use an indelible felt marker, a log crayon, or a nailed/stapled metal tag on the blaze.

5.4.2. Record Sample and Plot Attributes

5.4.2.1. Record Sample Attributes

The sample attributes are biogeoclimatic zone, subzone, and variant. Determine the BEC zonation of the site using the regional guide book. This is a field assessment and the BEC map should only be used as a guide.

5.4.2.2. Record Plot Attributes

The plot descriptors — elevation, slope position, percent slope, aspect, and site series — are determined for each plot.

5.4.3. Assess Tree(s) for Pathological (Path) Indicators

Note: The assessment of path indicators **must** be made for all trees in the sample plot **before felling neighbouring trees.**

Assess for the standard RIB volume and decay pathological (path) indicators. These are: conks, blind conks, frost cracks, scars, forks, crooks, large rotten branches, dead tops, root rot, and broken tops and their definitions adhere to the traditional ones of the British Columbia Loss Factor System. The objective is to maintain a system that is compatible with current and past inventories, but will also meet future needs. Path indicators and VRI loss indicators are identical, the exception being that the consideration of the time elapsed since the path indicator was created. The VRI loss indicator system does not recognize time. The general guideline for pathological indicators that describe stem damage, such as scars, forks, crooks, and dead and broken tops, is that at least 5 years must have passed since the damage was created. This guideline conforms to existing operational timber cruising, inventory audit, and volume and decay sampling rules for path indicators.

For each indicator on the standing tree, identify, estimate, and record the average height. For scars, record lower and upper heights and an average width.

Note: A reassessment of path is made for the felled tree, which will include much of the standing path but will also include indicators hidden in the crown or in the stem.

Do not confuse broken tops with forks or crooks, as this will affect tree height and the compiled taper equation volume.

Assess measurable secondary leaders for path indicators.

Candelabras are also recorded but are not considered to be path indicators.

General Procedures

1. Record path indicators for all sample trees.

Note: Record path indicators for dead trees also.

2. Enter the appropriate code for the path indicator. See Table A.1 for the appropriate code.
3. Enter a minus sign (–) if below high side ground level.
4. Estimate the position of each path indicator on the stem of each sample tree to the nearest 0.1 m.
5. Record path indicators for all measurable leaders from the tree base to the top of the leader.
6. If the path indicator is too numerous, i.e. 20+ conks over a 10 m length, to separate as individual items, record as one item. Make a note if this situation occurs.
7. For closed scars, record 0.1 cm width. For open scars, record average width of opening.

Table 5-2. Stem Analysis Path Indicator Codes.

Code	Description
CONK	Stem or root decay (conk)
BC	Blind conk
FC	Frost crack
SCAR	Scar
FK	Fork
CK	Crook
RB	Large rotten branch
DT	Dead top
BT	Broken top
CD	Candelabra

Conk Stem Decay Observed on Bole

Conks refer to the fruiting bodies (sporophores) of stem decay fungi and are definite and reliable indicators of decay. Typically conks are thick, hard, woody-like perennial structures. Only specific root, butt, and heart-rot conks are considered to be path indicators. Slash conks that occur on dead branches and wounds of living or dead trees are not considered path indicators. Fruiting bodies can occur anywhere on the main stem and/or branches, but they

appear most frequently around knots and on the underside of dead branch stubs and live branches. Record position on trunk.

Conk Root or Butt Rot Observed on Roots or Ground

Root rot refers to fruiting bodies that located on the roots and associated with stem decay and include decays such as *Phaeolus schweinitzii*. Typically, fruiting bodies are short-lived, soft, and fragile. Often you may be able to see an indication of root rot decay directly on the roots. Record "0" (ground level) as the length for any single or multiple root rot indicator.

Blind Conk

Blind conks are pronounced swellings or depressions around knots, usually caused by *Phellinus pini* (DDP) on conifers, and *Phellinus tremulae* (DDT) on aspen. Blind conks are definite indicators that decay is extensive in the tree stem. Find evidence of **conks** in the surrounding stand before recording blind conk as an indicator. Look for stem swellings and stem depressions thought to be where the tree attempts to heal over decay emerging through a knot or branch stub. Bright yellow to buff-coloured material can be observed by chopping into basal branch stubs. This form is most often found in the interior of the province. The project supervisor will direct crews regarding procedures for chopping into trees.

Note: Verifying the existence of blind conks is the only situation where we allow crews to chop into live trees on the plot.

Frost Crack

Frost cracks result from deep radial splitting of the trunk, caused by uneven expansion of moisture in the tree after a sudden and pronounced drop in temperature. The cracks usually originate at the base of the trunk and may extend many meters, following the longitudinal grain of the tree. The wound will often spiral up the tree following the movement of moisture. Frost cracks are often reopened and extended by wind stresses or refreezing. Repeated healing of the cambium produces pronounced callous tissue, giving a ribbed appearance to the wound.

Scar

A scar is an injury caused by external forces that damage the cambium or heartwood of the tree, exposing the tree to wood-decay fungi. A scar can occur anywhere on the main stem or root collar of the tree. Scars on branches or candelabras are not recorded.

A scar may be "open" meaning the wood is exposed, or "closed" meaning that the bark has grown over the injury. Old healed-over fire scars are recorded.

Fork

A fork is caused by significant damage to any measurable leader of a tree that results in more than one branch (leaders) competing for apical dominance. The damage to the leader from external forces, physiological factors, animals, or insects (weevil) exposes the stem to potential wood or decay fungi. The following conditions are **not considered forks:**

- natural branching in deciduous trees
- small sharply angled branches or spikes, unless associated with a noticeable offset or diameter change at the location
- flattening of the tree tops caused by wind or physiological conditions where no terminal leaders are evident
- candelabra branches

Crook

A crook is caused by significant damage (mechanical, physiological, animal, or insect attack) to the leader of a tree. Crooks potentially expose the wood to decay fungi. Crooks may still have the stub of the old leader and differ from forks by the absence of two or more leaders. To be recorded as a crook, it must meet the following conditions:

- the diameter of the main stem changes noticeably from the normal taper, and indicates that an injury has occurred
- the stem must be offset severely enough to indicate that damage has occurred to the main stem

Large Rotten Branch

Large rotten branches are defined as those with a diameter inside the bark greater than 10 cm at the base. They have obvious signs of heart rot and typically appear as short, rotten branches on overmature trees. They should not be confused with branches that have died through normal causes.

Dead Top

Any number of external injuries, physiological stresses, insects, or diseases can cause a dead top. The top should be obviously dead with no green needles or leaves present. Record the length to the base of the dead top (top of live crown).

Broken Top

A broken top is produced when an external force or condition causes the top of the tree to break away from the main bole. Wind breakage, snow damage, and mechanical damage from other falling trees commonly cause broken tops. Record the length to the break (estimate by folding back any jagged parts of the stem to form a complete stem).

Candelabra

A candelabra is a leader that was **not** created from direct damage to the original leader, but developed from abnormal branching.

5.4.4. Mark and Measure Standing Trees

Note: Complete the standing measures for all sample trees in the plot before the falling begins. It is vital that the path indicators are assessed prior to any felling so to match the stand conditions found by the VRI ground sampler.

5.4.4.1. Limb Branches and Remove Obstructions from Tree Base

Prepare sample tree by limbing lower branches. If possible, remove obstructions around the base of the tree.

5.4.4.2. Relocate and Mark the High Side of the Tree

High side is defined as the highest point of mineral soil around the base of the tree. If the tree has a pronounced sweep, logs, rocks, or boulders at the base, the point of germination will be high side.

5.4.4.3 Mark the Butt Taper Heights

Mark the butt taper (0.3, 0.6, 0.9, 1.3 m) heights above high side and around the bole with paint. Measure the butt taper height measurements parallel to the trunk (Figure 5-2).

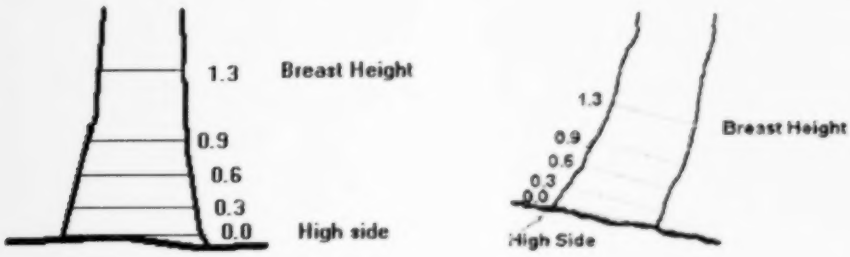


Figure 5-2. Butt taper Marks, in Meters, Above High Side.

Note: The data collection software allows for an optional DOB and DBT measures at a user defined height anywhere between 0 and 0.3 m. This optional height is not a NVAF standard.

5.4.4.4. Measure the Butt Taper Diameter Outside Bark (DOB)

For each of the butt taper heights measure the DOB with a diameter tape. Use two people to ensure the D tape is at right angles to the trunk. If there are obstructions or forks below 1.3 m, estimate the butt taper DOBs, (Figure 5-3).

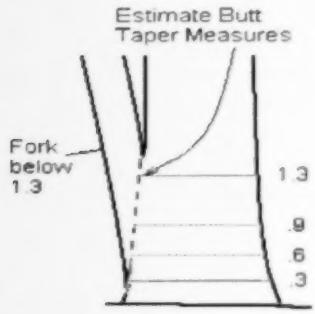


Figure 5-3. Estimation of Butt Taper DOBs in case of Forks.

5.4.4.5 Cut Bark Windows and Measure Double Bark Thickness (DBT)

With a chain saw or an axe cut bark windows at opposite sides of the tree stem at each butt taper point. When locating the sites to cut bark windows, attempt to avoid atypically thin or thick bark. For trees on steep slopes, it is acceptable to cut the bark windows on either side of the contour due to difficulty in reaching the upper butt taper heights on the bottom side of the tree. Measure both of the bark thicknesses at each taper point at a representative thickness and add them together to produce the double bark thickness (DBT), (Figure 5-4).

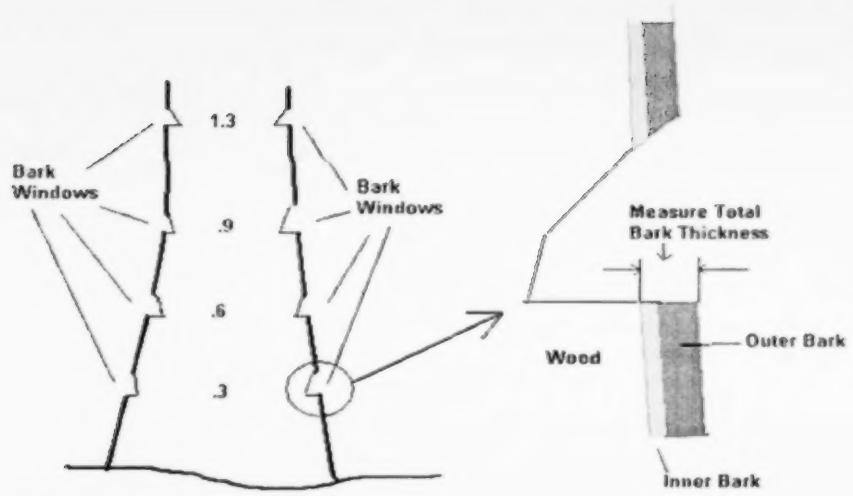


Figure 5-4. Bark Windows.

The bark on all but very young trees varies considerably over small distances due to small troughs and projections. The objective is to convert the DOB measure to a diameter inside bark (DIB) value by subtracting the DBT. Therefore, select a typical bark projection and measure from the cambium to the outer edge of the projection (Figure 5-5). Calculate a prorated bark thickness if bark is missing from a significant portion of the stem. For example, if bark is missing from 25% of the trunk circumference, then cut bark windows from the portion with bark and then reduce the double bark thickness by 25%.

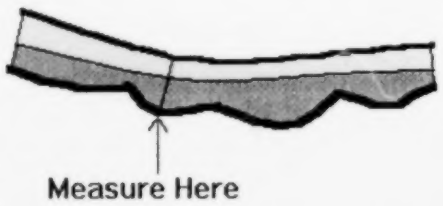


Figure 5-5. Selection of Site to Measure Bark Thickness.

5.4.5. Fall, Buck, and Measure Age of Trees

5.4.5.1 Fall and Limb the Tree

Ensure the crew moves to a safe distance when the sample tree is felled. On a hillside, the most favourable landing of the tree is across the hill, rather than up or down hill. Where possible, avoid falling trees across a stream or creek. The falling process is at the faller's discretion. Limb the sides and top of the tree stem.

5.4.5.2. Buck Below 1.3 m (Butt Taper Sections)

Buck the 0.3 m section and the 1.3 m sections of all sample trees. A 'cookie' is bucked at each of these heights. See section 6.11 for the cookie definition and instructions of cutting.

5.4.5.3. Measure Age

Buck a cookie (see section 6.11 for the cookie description) **from the top of the 1.3 m section,** instead of from the bottom of the 2.3 m section.

Count the age using the growth rings, marking 20-year increments with an indelible marker. This is an important measure and care must be taken to clean off a radius for an accurate ring count using a high powered hand lens. Estimate the number of years required for the tree to grow to breast height, and record as the age correction. A site index table is suitable for use.

If decay precludes an accurate ring count, then count the rings that are observable and measure the radial extents of both the counted and uncountable wood (Figure 5-6). Measure the sound wood at a point that reflects the growth rate for the missing section.

The handheld software will calculate the rings per centimetre of the counted wood and apply this factor to the uncountable wood to determine the stump age of the tree.

If the uncountable portion is localized at and around 1.3 m such that accurate age counts can be made adjacent to breast height between and including the 0.3 and 2.3 m sections, then count the age at the more accurate location.

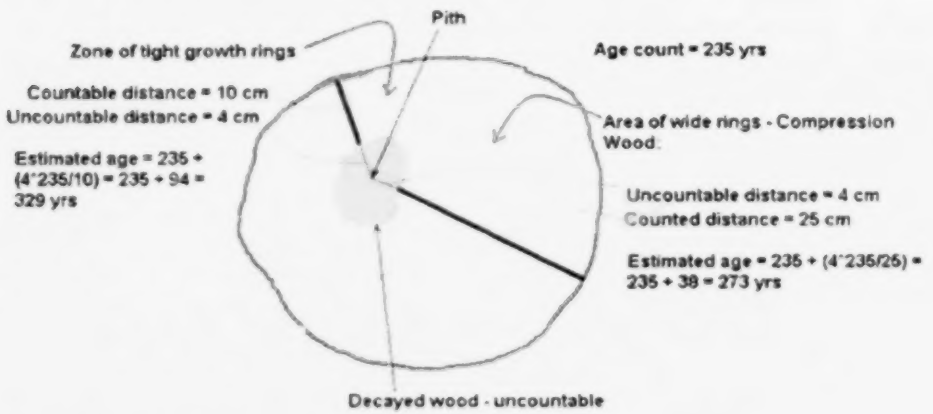

Pith
Zone of tight growth rings
Age count = 235 yrs
Countable distance = 10 cm
Uncountable distance = 4 cm
Area of wide rings - Compression Wood
Estimated age = 235 + (4*235/10) = 235 + 94 = 329 yrs
Uncountable distance = 4 cm
Counted distance = 25 cm
Estimated age = 235 + (4*235/25) = 235 + 38 = 273 yrs
Decayed wood - uncountable

Figure 5-6. Determining Age in Rotten Trees.

5.4.6. Mark and Measure Felled Trees

5.4.6.1. Reconstruct the Tree if Broken During Falling

Before limbing the upper portion of the tree, look for the tree top and forks. The top of the tree can readily break off during the felling process and be difficult to locate. Consequently, it's easier to identify the top before the cut limbs obscure the ground.

5.4.6.2. Run Measuring Tape along Stem of Tree

Attach the metric tape to the butt of the felled tree at 1.3 m and run it up the tree stem to mark sections and defects. To avoid measurement error, ensure the 1.3 m mark on the tape is lined up exactly with the trunk's breast height.

5.4.6.3. Identify Primary and Secondary Leader(s)

Identify the Primary Leader

The primary leader is determined by leader length and will be the longest leader, all other leaders are potential secondary leaders, (Figure 5-7).

Figure 5-7. Primary Leader Identification.

Identify the Primary Leader if Broken Top Present

The one exception to the rule of the primary leader being the tallest leader is in the case of a broken top. If a tree has produced new leaders as a result of a broken top, the determination of the primary leader is based on projecting the old broken off top and comparing its size to the new leaders. As a guideline, if a new leader's height and DIB (diameter inside bark) at its base is greater than 75% of the projected broken top then it is a primary leader candidate, (Figure 5-8).

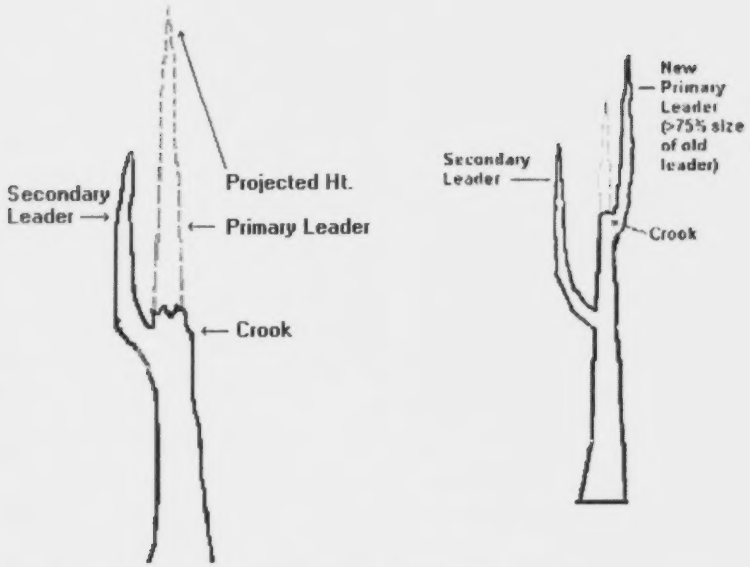


Figure 5-8. Identifying the Primary Leader if a Broken Top.

Identify Secondary Leader(s)

The secondary leader is greater than 3 m in length from its base to its upper utilization point (Utop) of 10 or 15 cm (depending on tree age and location) diameter inside bark (DIB). The base of the leader is the bottom point of the forked section of the primary leader. Secondary leaders are measured if the following applies, (Figure 5-9):

- originates from the primary leader,
- originates above breast height,
- is alive,
- meets the length criteria.

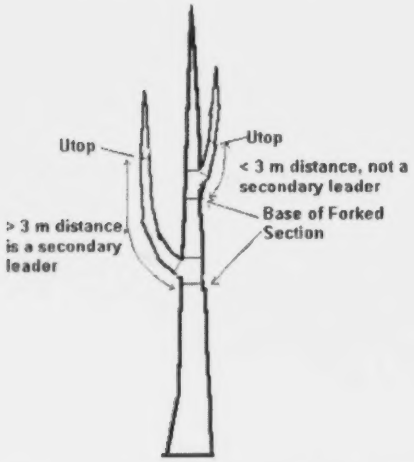


Figure 5-9. Secondary Leader Merchantability.

Assign a leader number to a secondary leader before marking the individual sections. Estimate the approximate height of the leader's start height (point of origin on the primary leader). In the case of multiple secondary leaders, the identity of the leader is determined by its approximate start height (Figure 5-10).

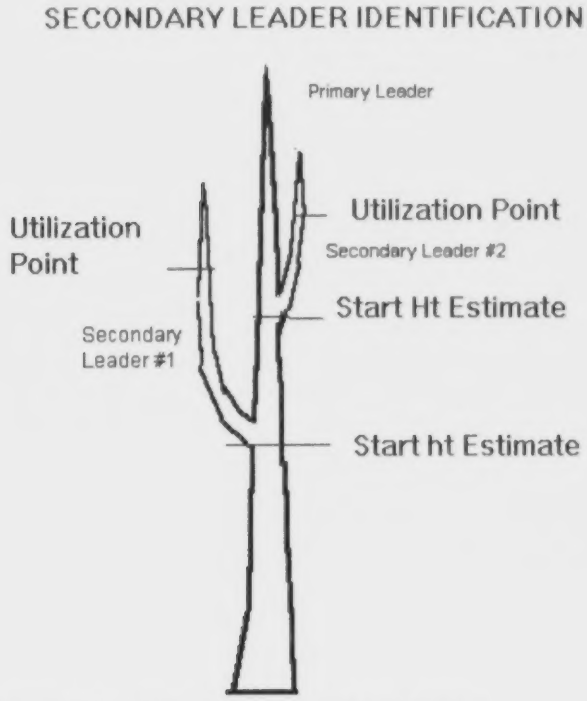


Figure 5-10. Secondary Leader Identification.

5.4.6.4. Locate Heights of Primary and Secondary Leaders

Heights are measured to the nearest 0.01 m.

Primary Leader

Crown height

Measure the base height of the live crown on the primary leader. When determining the base of the lowest contiguous live crown, do not consider forks or epicormic branches. The height is normally the location on the stem where live branches occupy about 75% of the stem circumference. If the crown is asymmetrical, select a height equivalent to the average crown. Dead trees will not have a live crown and should be given a live crown height .01 m below the tree or broken top height.

Utop height

Determine the location of the Utop on the primary and secondary leaders by:

- estimating the approximate location
- chopping a bark window
- measuring the bark thickness

- calculate the double bark thickness
- adding the DBT to the Utop DIB

This process provides the Utop diameter outside bark (DOB). Then, locate the Utop DOB on the leader by selecting the upper most point on the stem that will give the correct Utop inside bark diameter. Ensure the bark window is less than 30 cm from the final utop position. Because of abrupt changes in leader taper due to branch swellings, forks, or crooks, there may not be an actual Utop DIB. If this is the case, provide a best estimate of the Utop.

Note: Utop DIB is either 10 or 15 cm and depends on location and tree total age. Coastal trees > 120 years of age have a 15 cm Utop DIB and all other trees have a 10 cm Utop DIB.

Broken Top Height

If the primary leader has a broken top, fold the top down to produce an even height as per the VRI ground sample process and measure the height to the break point. Then, estimate the length of the missing section and add it to the break height to produce the total height. The estimate can come from a measurement of the broken top if located or by assessing intact trees in the vicinity, (Figures 5-8 and 5-11).

Broken tops can be differentiated from forks or crooks by comparing the size of old broken off leader to the new leaders that have formed as a result of the break. If the new leader's height and DIB at its base are less than 75% of the original leader's projected height and DIB at the break, a broken top is called; if the new leader is greater then 75%, then a fork or crook is called.

Trees with broken tops require an estimate of projected height beyond the break. In contrast, the height of a forked or crooked tree is that of the tallest leader's terminal bud. Hence, using a projected height versus an actual height will profoundly affect the volume estimated by the taper equations.

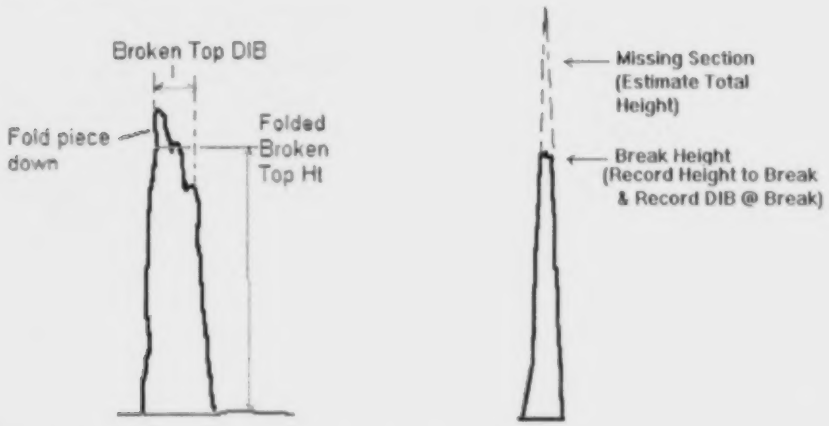

Broken Top DIB
Fold piece down
Folded Broken Top Ht
Missing Section (Estimate Total Height)
Break Height (Record Height to Break & Record DIB @ Break)

Figure 5-11. Broken Top Height and DIB Measurement.

Broken Top Diameter

Measure the diameter inside bark of the break.

Total height

- Measure the total lengths of the primary and secondary leaders.
- In the case of trees with flat tops that are not broken as in the case of suppressed or very old trees, measure the top at a point where the top starts to level off.
- Mark the leader tops with ribbon or a dot of paint.
- In the case of a top that cannot be located and the missing portion likely amounts to a very short length of < 1m with a DIB <1 cm, then estimate the length of the missing section and add it to the measured length and record this sum as the total height. In many cases, the missing portion amounts to part of one year's leader growth and ranges from 20 to 50 cm of length. The sampler should be confident about their estimate.
- In the case of a top that cannot be located and the missing portion likely amounts to a long length of >1m and a DIB > 1cm, then measure the actual length and record as a broken top. Estimate the missing portion and add it to the measured length and record the sum as the total height. Do not record a broken top path call.

Note: Differentiating between a broken top and a fork or crook is vital in determining tree height and the subsequent estimation of gross tree volume through the taper equation.

Secondary Leader

Utop height

Apply the same procedure as for primary leader.

Total height

Top height for the secondary leader is taken from high side to the tip of the top of the secondary leader.

Note: Secondary leaders do not require a projected height.

5.4.6.5. Locate, Mark, and Measure Fork(s), and Crook(s)

Note: Forks, and crooks must be properly identified at this stage in the NVAF sample.

See section 3 for the definition of the crook and fork path indicators.

The principle of sectioning out forks and crooks is to:

- Ensure the volumes for the preceding and subsequent sections of the tree are relatively accurate in terms of an even change in taper for their sections.
- To readily capture decay arising from the old broken top origin of the fork or crook.

Always mark the bottom and top of a crook or forked section regardless of the length of the secondary leader. The bottom mark is made where the swelling of the trunk begins. Mark the top immediately above the crotch of the fork or crook. If the other leaders of a fork meet the secondary leader requirements, then place the top section marks of the leaders at the same height as the primary leader section (Figure 5-12).

Forks and crooks are also sectioned on secondary leaders.

Forks and crooks are not sectioned below 1.3 m.

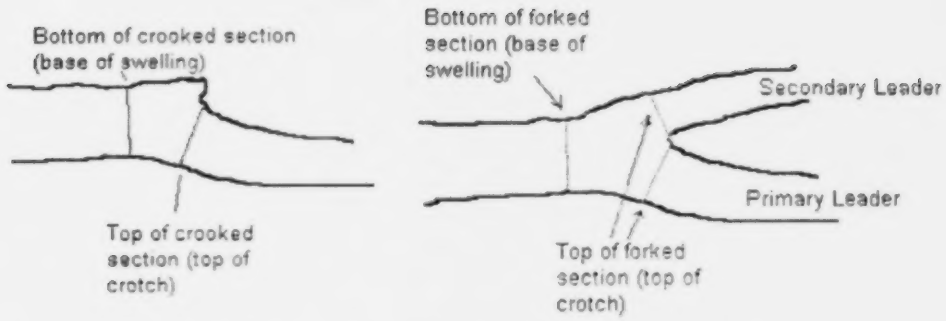

Bottom of crooked section (base of swelling)
Top of crooked section (top of crotch)
Bottom of forked section (base of swelling)
Secondary Leader
Primary Leader
Top of forked section (top of crotch)

Figure 5-12. Marking the Top and Bottom of Forked or Crooked Sections.

Note: If a sample tree has a secondary leader in the butt section (below 1.3 m), measure only the leader that is identified as the sample tree. If the secondary leader belongs to the same tree, then record the secondary leader as a path indicator.

5.4.6.6. Identify and Measure Path Indicators

Scrutinize all the tree sections for path indicators using the list of standing path indicators as a guide. See section 3.0 for definitions.

Locate **all** path indicators. Identify each indicator, measure and record the lower and upper heights of all indicators. Record the average widths of scars. If numerous indicators such as conks or scars occur every few centimetres along the stem, record the height range and make a comment. In determining the height of the primary leader, differentiate between a fork or crook and a broken top.

Path indicators that were called incorrectly as standing path are corrected for the felled path. For instance, a standing frost crack found to be a scar once the tree is felled is to be identified as a scar.

Try to identify the decay organism associated with a conk. If a conk associated with heart rot is identified in a branch, record the height of the base of the branch as the height of the conk. Common conks associated with heart rot are *Echinodontium tinctorium, Phellinus pini, Fomitopsis pinicola,* and *Phaeolus schweinitzii* (the last usually occurs on the ground near the base of the tree). For *Phaeolus schweinitzii* occurring on the ground, record the height as 0 m

5.4.6.7. Mark Significant Taper Changes

If the diameter taper of a section is not even from one end to the other end and the taper change is not due to a fork or crook, then adjust the section length to better capture the section volume. Alter the sectioning to allow for a section to encompass the area of significant taper change. This is done to capture the change in volume due to the decreased or increased section diameter (Figure 5-13).

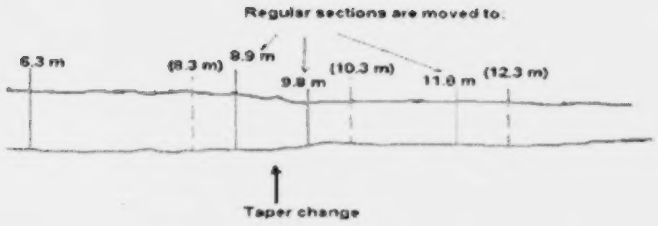


Figure 5-13. Sectioning for Taper Changes

5.4.6.8 Mark Off Sections Above 1.3 m

With paint, mark off sections. The standard section length is 2.0 m. The first section above breast height is section number 5, and the top of this section will be at 2.3 m (2.0 m above the 0.3 mark) (Figure 5-14).

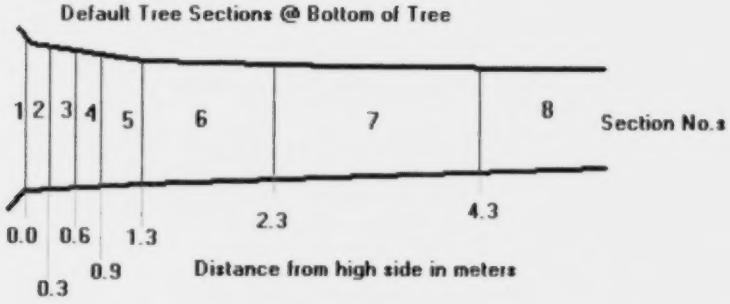


Figure 5-14. Sectioning the Bottom of the Tree.

Section lengths can be extended for up to half of the default length (i.e., 1.0 m). Sections are extended to meet the bottom section of a fork, crook, top, or broken top. The default section length of 2.0 m is resumed above forks and crooks. Mark section cumulative lengths and leader number at the top of each section. **Do not section above the leader Utop height.**

Secondary Leader

Divide the secondary leader into sections using the same process as the primary leader. The top of the first section of the secondary leader will always be the same height as top of the forked section on the primary leader.

Mark and section all crooks and forks on the secondary leader, but **do not section secondary leaders off secondary leaders,** (Figure 5-15).

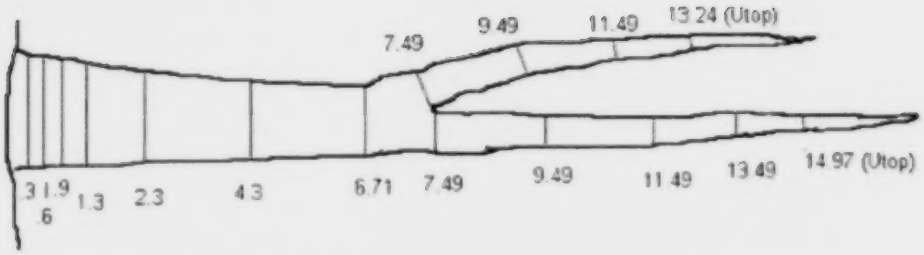


Figure 5-15. Marking the Sections

5.4.6.9. Assign Leader Number(s) to Secondary Leaders

Using the leader start height as a guide, assign the appropriate secondary leader number to the forked primary leader section.

5.4.6.10. Buck Sections

After the tree is marked and the path indicators have all been located, buck out all of the tree sections including the Utop section, with the exception of the .6 and .9 sections.

5.4.6.11. Buck "Cookies"

Cut a 5 cm thick cross-section (a "cookie") off the bottom of every section. Identify each cookie by marking the cumulative length and the tree and leader number on the face of each cookie (Figure 16).

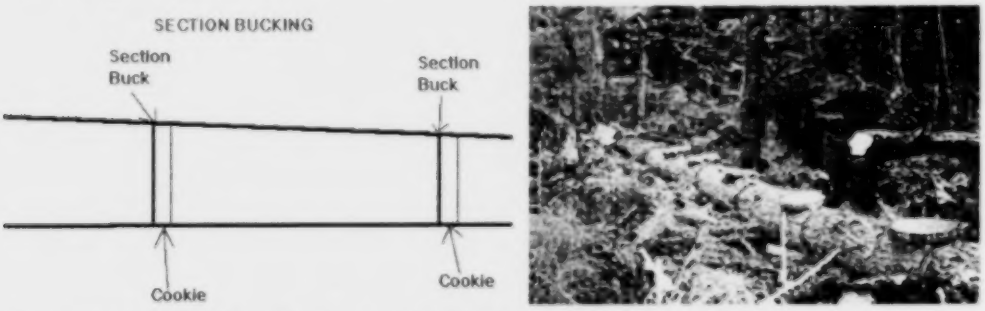


Figure 5-16. Bucking the Section and Cutting Cookies.

5.4.6.12. Measure DIB (Diameter Inside Bark) of Each Section

Regular Shape

Start measuring the bottom-most section of the tree (starting at sections above 1.3 m) and work towards the top. Measure the lower face of the cookie cut from the bottom of the next section.

Determine the longest axis and mark the two end points with an indelible felt pen. Then at right angles (90°) to the long (width) axis mark the short (breadth) axis, (Figure 5-17). Having long and short axes will create an elliptical shape. Using a carpenter's tape, measure to the nearest 0.1 cm.

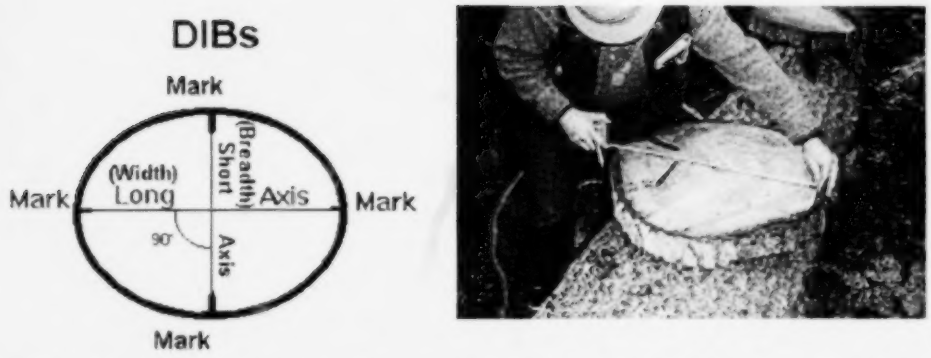


Figure 5-17. Measuring the Cross-Section Diameter Inside Bark (DIB), Short and Long Axes.

Irregular Shape

If the shape of the cross-section is severely distorted then determine if decay has caused the irregular shape

- Decay: If the cause **is decay,** "rebuild" the decayed portion and measure the DIB to the edge of the "rebuilt" portion (Figure 5-19).
- Void/Irregular Shape: If the distortion is **not due to decay** but to other causes such as large knots, irregular cambial growth, extensive weathering, or scar voids, then smooth out the irregularity into a more regular elliptical shape (Figure 5-18). The sampler should assess the overall section taper when making their decision about the final shape of the section.

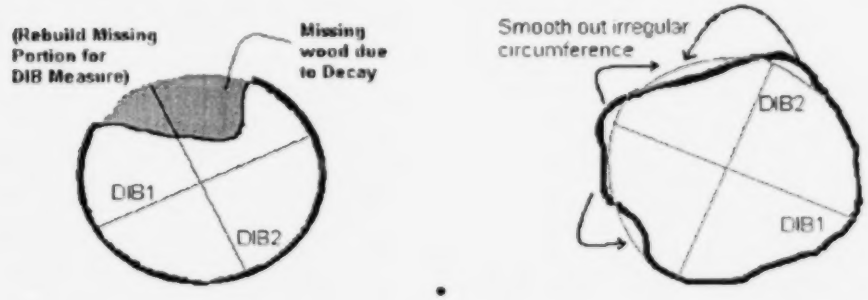


Figure 5-18. Measuring DIB of an Irregular Cross-Section.

5.4.6.13. Identify Decay Characteristics

Stains

Stains and discolourations may be caused by incipient decay, by chemical reactions, and by stain-producing fungi.

Stains caused by non-woodrotting fungi are usually confined to the sapwood of the tree, whereas those caused by incipient decay are usually associated with the heartwood. Although stains do not affect the strength of wood, the unsightly discolourations are

sometimes commercially unattractive, which may be reflected in a lower grade. Decay and stain are often found together because they develop under the same conditions.

Recognizing Decay

Wood-rotting fungi cause decay of wood. Hyphae, which constitute the vegetative stage in the life cycle of the fungus, penetrate the cell walls of wood and dissolve various constituents, which then nourish the fungus. These physical and chemical changes cause the wood to disintegrate in a process called decay.

Stages of Decay

The three stages of decay are incipient, advanced, and final (Figure 5-19).

1. In the *incipient* (initial or early) stage, affected wood *may appear* quite sound and hard. The only visible evidence of attack, if any, is a slight or pronounced change in colour. The degree of discolouration varies with the species of fungus involved and, sometimes, with the species of tree affected. Incipient decay often appears as a light to dark reddish-brown, olive, or purple streaking (or banding) of the heartwood. In some decays, the delignifying action of the fungus bleaches the wood. In recent infections, incipient decay may occur alone, time having been insufficient for advanced stages to develop. **For the purposes of NVAF sampling, incipient decay is defined as wood that is likely attacked by wood rotting fungi but no loss of fibre strength can be detected.**
2. At the *advanced* stage (large or typical) of decay, the strength of the wood has been so seriously affected that it is easily broken and can often be crumbled between the fingers. When tested with a knife, wood affected by advanced decay is soft and has a punky or brash texture. To test for these symptoms, use the point of a knife or an axe.
3. In the *final* stage of decay, destruction of the heartwood may be complete, leaving only a shell of sound sapwood.

Measurements are taken of the advanced and final stages of decay.

Advancement of decay varies with the individual tree and with the species of fungus. In older infections, incipient decay appears at the advancing margins of visible decay, separating the advanced decay from sound wood. This advancement occurs radially and from the advanced decay to the sound wood. Longitudinally, the incipient decay can extend a few centimetres or several meters from advanced decay; radially, it extends usually 2 or 3 cm.

Decay may be classified by the type of wood attacked (heart rot or sap rot) or by its location within the tree (root rots, butt rots, trunk rots, or top rots).

Multiple infections often occur in the same tree: butt rot caused by one fungus gaining access through roots, trunk rot in the second log caused by another fungus gaining entrance through a scar, and top rot caused by a fungus entering through a broken top.

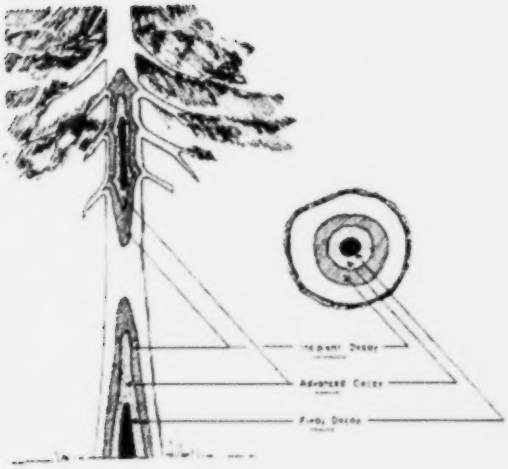


Figure 5-19. Various Stages of Decay in an Infected Tree.

Entrance

Determine the entry point of the decay organism. Examples are scars, broken branches, conks, forks, crooks, broken tops, or roots. If the entry point is not obvious, record it as unknown.

Descriptors

Decay descriptors identify the pathological characteristics of the decay. Examples are pits, flecks, strength, colour, and shape. NVAF sampling does not normally require a pathological description of the decay and instead relies on an average (or compound) description to be selected from a list of common compound descriptors.

Examine the most advanced portion of the decay in the tree and select the most appropriate descriptor.

Decays are classified into two broad groups according to their effect on wood: white and brown rots. Both types of decay may appear in the same tree, with brown rots usually following the white rots. This classification is used for the possible recovery of pulp from the cellulose of white rots. No cellulose can be recovered from brown rots.

White Rots

White rots refer to a group of fungi that decompose lignin. The wood is generally reduced to a white, spongy mass, to white pockets or to a white stringy or friable condition varying in colour and form. Certain white rot fungi produce decays of colours varying from light to dark brown that can resemble brown rots in appearance.

Brown Rots

Brown rots result from fungi that primarily decompose the cellulose and its associated pentosans, leaving the lignin more or less unaffected. Their colour, always brown, is formed by the residual oily-brown or black derivatives of the lignin. The wood is reduced to a brown carbonaceous mass, often breaking into cubes, from which the term "brown cubical rot" is derived.

The classification of "brown-coloured" will help overcome the difficulty of differentiating decays in the field that are neither white nor brown cubical.

Brown-Coloured Rots

Brown-coloured rot refers to all brown rots that are not cubical in appearance. They may be yellowish, tan, or light brown and stringy or fibrous.

If possible, determine the species of the decay organism. If the species is not associated with a known conk, record it as unknown.

5.4.6.14. Identify Decay by Section

Starting with the bottom-most section, examine the surface of the cookie for discoloured or decayed wood. Outline areas of possible decay, then crack open every section cookie radially with an axe and scrutinize for decay. Crack the cookie into quarters and pick at the fibre with a knife to determine fibre length and strength with a particular focus on the areas initially outlined.

Measure decay in each section with the exception of the .6 and .9 sections where interpolation can be used.

Identify Decay Area With the "Pick Test"

Use the "pick test" to determine the cross-sectional extent of decay. A sharp pointed knife is used to obliquely pick at the wood fibre on the radial edge to determine the length and strength of wood fibre, where weak and short fibres are candidates for decay. This is a subjective test and it is recommended that the sampler start off in areas of obvious sound wood in an effort to calibrate themselves as to what would constitute sound wood. In areas of advanced decay, the pick test will readily determine short and weak fibres. However, great care must be taken for incipient decay and its boundary between advanced decay.

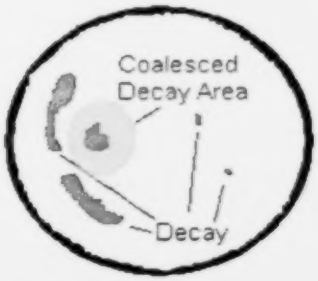
Note: Measure only final decay and advanced decay indicated by the presence of short, weak fibres. **Do not measure incipient decay**.

Some decays are characterized by pitting such as *Phellinus pini* (white pits) or to a lesser extent *Echinodontium tinctorium* (orange brown pits). For these two decays only, the boundary between decayed and undecayed wood is not determined by wood strength but by the presence or absence of the white pits (Figure 5-20). If pitting is intermittent, measure using the approach used in cases of extreme intermingling of decay and sound wood described below.

Figure 5-20. Phellinus pini Pitted Decay

Coalesce the Decay Area

If the decay is not obvious or has an irregular cross-section, use a marker to delineate the cross-sectional boundary of the decay. Take care to identify areas of sound wood within the decayed area. Coalesce the decay into a more regular elliptical shape for measuring with long and short axes (Figure 5-21).



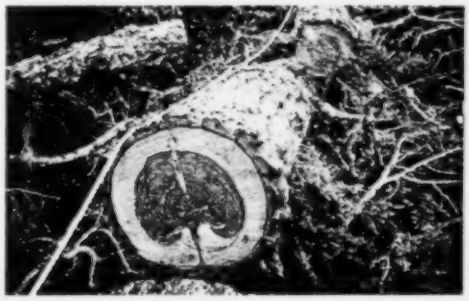


Figure 5-21. Coalesce an Irregular Decay Shape.

5.4.6.15. Measure Decay

At this stage, look over the sample tree and decide on the most efficient strategy to describe, measure, and record the decay(s) in terms of shape and mix.

Note: Only one attribute can be set for each decay characteristic. **It cannot be changed part way up the tree.** If the wrong attribute is chosen, the sample may fail or cause the sampler to take extra effort and time.

If decay is present, record it for every section in which it occurs throughout the tree, from high side to the tip of the leader. If the decay ends in a section, then occurs elsewhere in the tree, it will need a separate identity. For example, if the same decay occurs in the primary and the secondary leaders, give the decay in the secondary leader a separate identity and description.

Shape

Decay shape can be either solid or ring-shaped and is always measured as an elliptical form. Decay shape often changes form throughout its length and this change can make measuring

difficult if the most appropriate shape is not determined from the start. Once the shape has been decided it cannot be changed. To determine the easiest shape to measure, take a look at the behaviour of the decay in the sections further up the tree.

If the decay is a **solid shape,** measure the diameter of the decay in the same way as the section DIB for the sections with long and short axes.

If the decay is a **ring shape,** measure the diameter of the decay in the same way as the solid shape. However, for each axis record both the inner and outer measures (Figure 5-22).

Note: A ring-shaped decay can be converted to a solid by measuring the inner diameters as minimal lengths of 1 mm by 1 mm.

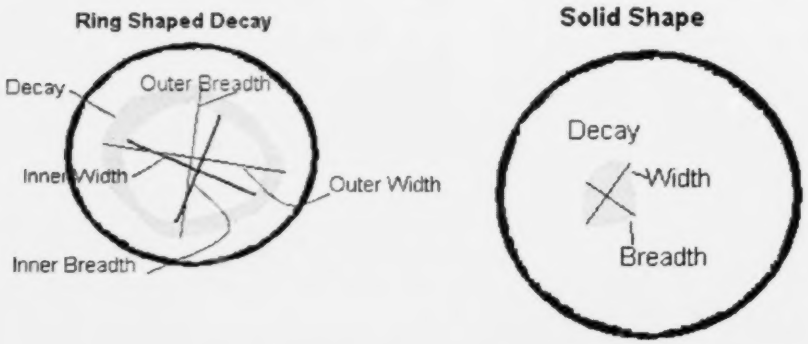


Figure 5-22. Measuring Diameters for Ring-and Solid Shaped Decays.

Mixed Decay

Decays are considered to be mixed if two or more decays are so intermingled that they are impossible to separate. Frequently, decays can be separate in one section and mixed in another. A decay that has been set as a separate decay can be difficult to measure if intermingled with other decays. Therefore, it is important to identify from the onset the appropriate strategy in recording mixed decay. It is recommended to create a mixed decay due to the sampling efficiencies that can be gained. Estimate the percentage of the cross-sectional area occupied by the mixed decay to the nearest 5%. The mixed percentage is section-specific. If one decay ends before the other(s) in the mix, set the percentage to 1% for the duration of the mix (Figure 23). **Do not mix voids and decays together.**

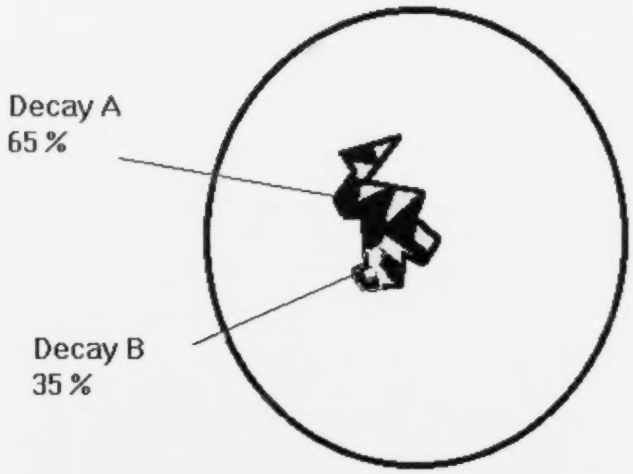


Figure 5-23. Estimating Proportion of Mixed Decay.

Measurement if Extreme Intermingling of Decay and Sound Wood

In some extreme cases, the decay will be intimately intermingled with sound wood which would otherwise require extensive cookie cracking and picking. Not only can the determination of decay be time consuming, but it can also be inaccurate due to the difficulty in piecing together the cookie from the numerous breaks. A quicker more accurate method would be crack the cookie into quarters, pick the wood and estimate a percentage of decay within the area of intermingled decay and sound wood. Measure the diameters of the overall area of intermingled decay and sound wood and reduce one axis by multiplying it by the decay percentage estimate. For example, if the overall area of intermingled decay and sound wood is 32 by 25 and the percentage of decay within this area is 75%, then multiply 32 by .75 and record the measurements 25 by 24. Leave an audit trail by writing the percent estimate of decay on the cookie (Figure 5-24).

Figure 5-24. Decay Estimation for Extreme Intermingling of Decay and Sound Wood.

5.4.6.16. Measure Voids

Voids are described as losses to sound wood that is not due to decay. They are subdivided into voids in the interior or exterior of a tree. **At present, flute voids are not measured operationally.**

Interior Voids

These consist of ingrown bark, insect damage (holes or cavities bored in sound wood by insects) and pitch pockets. Interior voids can be anywhere in the tree, from the high side to the Utop. They are measured the same as decay is, by coalescing into an elliptical shape and measuring long and short axes. To determine the length of the internal void, follow the process for intermediate bucking in Section 6.18. (Figure 5-25).

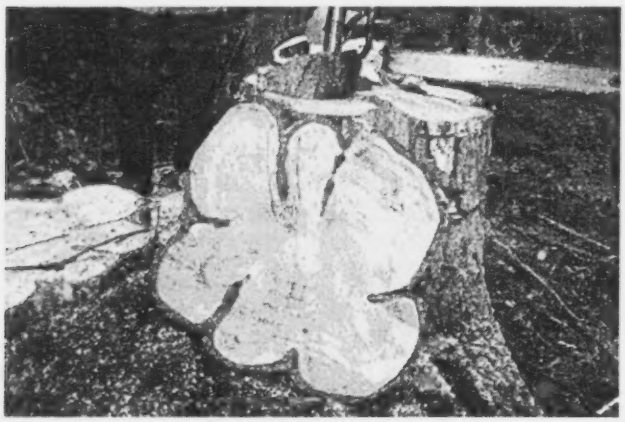


Figure 5-25. Bark Inclusions.

Exterior Voids

These result from scars or fluting at the base of a tree. **Measurements are generally only done for butt taper sections (high side to 1.3 m).** This is because irregularities in the circumference of sections above 1.3 are smoothed out through the DIB measurement process, (see Figure5-18) whereas the DOB measures in the butt taper include these irregularities. In some cases, scar voids may be measured above 1.3 m if they occur in the middle of a section length (see hidden decay measure, Figure 5-30) or where the scar void has such a substantial affect on section volume that would not be picked up through the normal DIB measure process.

The area of the void is coalesced into an ellipse, the same as for decay, (Figure 5-26). The length is measured directly from the tree, using the length of the start and end of the void.

Flutes do not need to be measured for NVAF purposes.

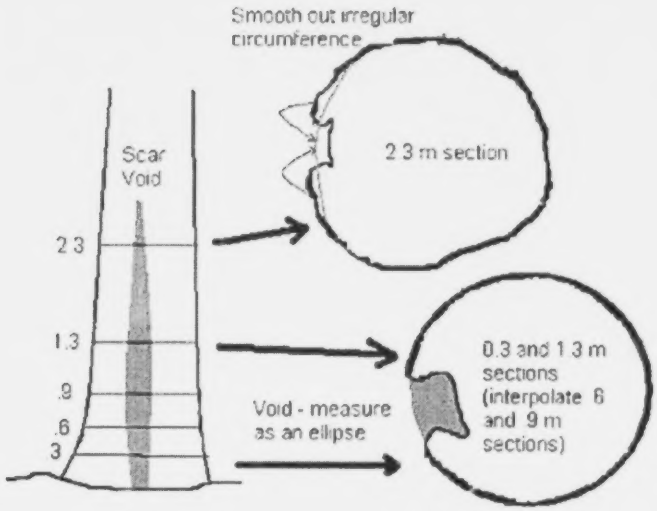


Figure 5-26. Measuring Exterior Voids.

Decay Interpolation Between 0.3 and 1.3 Heights

When decay is found at the 0.3m and 1.3m sections of a tree, the width and breadth of the decay must also be recorded for the 0.6m and 0.9m sections. The 0.6 and 0.9m sections do not have to be bucked to determine the width and breadth of the decay, this can be determined by pro-rating the measurements taken from the 0.3m and 1.3m sections, (Figure 5-27).

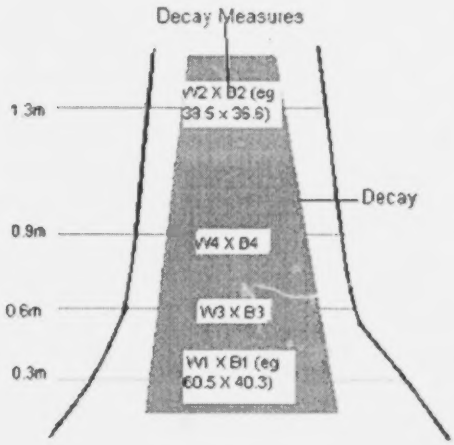


Figure 5-27. Interpolation of Decay.

1. To determine the rot width at 0.6m, take the two largest measurements from the 0.3 and 1.3m sections, and use the following formula: W3= W1-((W1-W2)***.3**)
2. Using the diagram above, the following numbers would be used 60.5-((60.5-38.5)***.3**) = 53.9cm, where 53.9cm is the rot width for the 0.6m section.

3. To determine the breadth for the **0.6m** section, take the smaller two measurements from the 0.3m and 1.3m sections and use the same formula with these measurements:B3 = B1-((B1-B2)*.3)
4. Using the measurements from the diagram, the formula would read: 40.3-((40.3-36.6)*.3) = 39.2cm
5. To determine the rot measurements for the **0.9m** section, the formula would read: W4=W1-((W1-W2)*.6) and B4=B1-((B1-B2)*.6), or using the measurements from the diagram, 60.5-((60.5-38.5)*.6)=47.3cm and 40.3-((40.3-36.6)*.6)=38.1cm

5.4.6.17. Determine the Length of Decay by Section

Decay length is measured relative to the top of each section by measuring the distance from the bottom and top of the decay to the top of the section, (Figure 5-28).

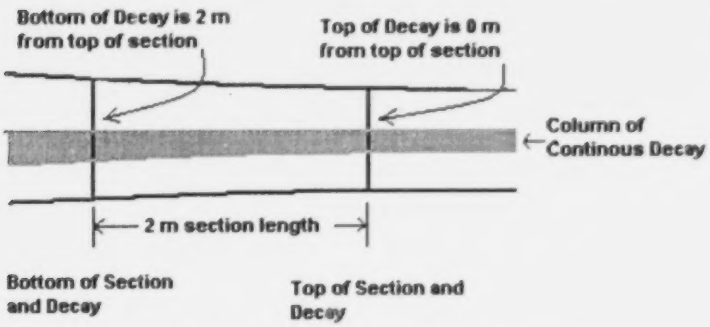

Bottom of Decay is 2 m from top of section
Top of Decay is 0 m from top of section
Column of Continous Decay
2 m section length
Bottom of Section and Decay
Top of Section and Decay

Figure 5-28. Measurement of Decay Length Within a Section

Intermediate Bucking

If the decay is not evident at both ends of the section, determine the length of the decay within the section by making a regular series of intermediate bucks, as follows:

Make the first buck halfway along the section. If the decay is still evident, make the next buck halfway along the remaining section, and so on. The maximum unbucked length should be approximately 25 cm. The preferred method of making the intermediate bucks is to cut a wedge shaped piece out of the section without cutting through the section (Figure 5-29).

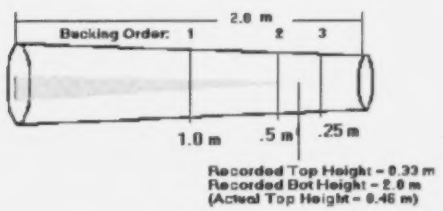


Figure 5-29. Recording Length of Decay Ending in a Section.

5.4.6.18. Check Path Indicators for Hidden Decay

All path indicators below Utop must be cut into and checked for hidden decay unless if decay is already evident. A typical situation is a scar on a section that otherwise does not exhibit decay. A pocket of hidden decay could be present beneath the scar.

Buck through the section, halfway along the path indicator. If decay is present, then measure the decay diameters at this buck. Make a buck at each end of the path indicator, then follow the regular intermediate bucking rules to determine the length of the decay in the section (Figure 5-30).

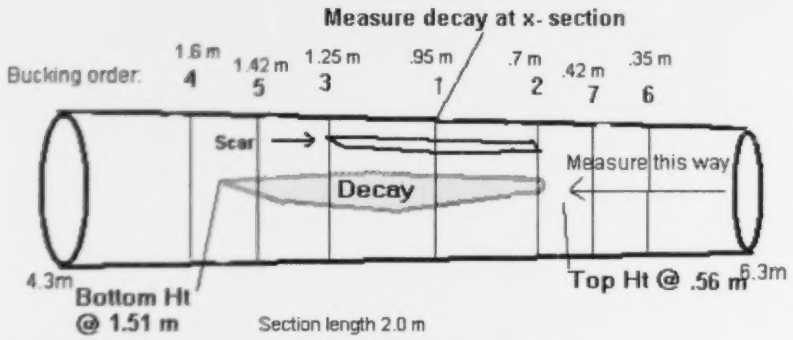


Figure 5-30. Bucking and Measuring Hidden Decay.

5.5. Data Edits and Processing

MSRM requires the submission of clean data using the volume and decay data collection software. The data is relatively error free, but may contain some small nonfatal errors that must be fixed prior to submission to MSRM. Most errors can be identified through a review of the decay reports produced by DVHost portion of the volume and decay data collection software.

5.5.1. Deletion of Unwanted Trees

Due to data entry errors or a failure to initially section the tree correctly, some trees are re-entered as new version of the same tree. The convention is to renumber the tree by adding 100 to the tree number. Previous versions of the same tree should be deleted prior to data processing and the DVHost software does allow for the selective uploading on individual trees from the handheld.

5.5.2 Ensure consistency of broken top attributes

Broken top information is entered in separately for tree height, felled path and as a section. All three sources must be made consistent in terms of path identity, height and broken top diameter. Since there is a strict definition for the broken top path indicator, it is possible to have a broken top height and as a section but not as a path indicator.

5.5.3. Ensure all decay length information is entered

The top height and bottom height attributes that are collected and used to calculate decay length in a section can sometimes be in error particularly for the base of secondary leaders.

5.5.4. Ensure decay attributes are entered

Essential decay attributes that affect decay volume can inexplicably be absent and are decay shape and type.

6.0 NVAF Data Compilation

6.1 Model Based

6.1.1 Introduction

This section outlines the tasks required to compile tree net merchantable volumes from the destructive stem analysis and VRI ground sample data sets and to calculate the NVAF and its statistics.

The model based estimation uses an assumed model to estimate population parameters. The model used for NVAF is the ratio of actual volume to the estimate of volume where volume is merchantable net decay and waste. An optimal weight, the *P* value, is derived to minimize the variance of the ratio.

The model method is based on the assumption that the sample trees have been selected without bias.

6.1.2 General Procedures

The general procedures for data compilation and NVAF calculation are outlined sequentially. The detailed procedures follow further in the section.

1. Compilation of the estimates of tree volume
   - Assemble sample information required to run the compiler.
   - Determine appropriate source of the inputs for the taper equation.
   - Compile tree volumes to VRI sample compiler standards
2. Compilation of the actual tree volumes
   - Compile volumes
   - Assess for errors in data
3. Merge the two volume datasets.
4. Calculate the model relationship.
   - Calculate the optimum 'p' value.
   - Calculate the model weight.
5. Calculate the NVAF.
6. Calculate the NVAF statistics.

6.1.3 Detailed Procedures

6.1.3.1 Compilation of the Estimates of Tree Volume

The current standard is the use of the SAS based VRI sample compiler to determine tree volume. The VRI sample compiler utilizes the BEC based taper equations, a facility to deal with broken tops and uses net factoring to estimate decay and waste losses.

Assemble Sample Information Required to Run the Compiler.

The essential sample attributes not found on the VRI raw data file are the administrative unit and biogeoclimatic zonation. These attributes are required as inputs for the BEC based taper equation.

Use Appropriate Source of the Inputs for the Taper Equation.

The primary inputs for the taper equation are species, dbh and height and there are two sources for this information: the cruiser estimates and the destructive sample. Typically, the NVAF height and dbh attributes are used as the inputs to the taper equation.

Compile Tree Volumes to VRI Sample Compiler Standards

Use the SAS based VRI sample compiler to compile tree volumes or a similar compiler that complies with the VRI compilation standards.

6.1.4 Compilation of the Actual Tree Volumes

The current standard is the use of the MSRM TIB (SAS based) volume and decay tree compiler. This compiler uses the DVHand data files as input and produces a standard set of output files.

Compile Volumes

Use the MSRM TIB volume and decay tree compiler.

Assess for Errors in Data

The volume and decay data collection software, DVHand and Host, produce relatively clean data files but can allow some errors to pass undetected. The errors that are critical to the compilation of wood volume are:

- Section gross wood diameters: identify and confirm diameters that increase with increasing tree height.
- Section decay diameters: identify and confirm diameters that exceed gross section diameters.
- Section decay length: identify and confirm decay lengths in the base of the primary and secondary leaders.
- Broken top height and diameter: confirm that the broken top height and diameter match the penultimate sections height and diameter.
- Upper (Utop) utilization height: confirm that there is a section ending at the Utop inside bark diameter.
- The NVAF tree species match the VRI ground sample tree species.
- The NVAF tree numbers match the VRI ground sample tree species.

The volume and decay tree compiler has a limited facility to identify potential data errors primarily in terms of section diameters that exceed expected limits. For example, the compiler will produce error messages identifying the section diameters that increase with height or decay diameters that exceed the section diameters.

6.1.4.1 Merge the Two Volume Datasets

Merge the dataset containing the estimates of tree volume produced by the VRI sample compiler with compiled volumes produced by the volume and decay tree compiler. The merge attributes are:

- VRI ground sample number and the region, compartment and sample number of the destructive sample data.
- The plot and tree number of both datasets.

6.1.4.2 Calculate the Model Weight

Calculate the Optimum P Value

1. Calculate the unweighted NVAF ratio

$$R = \frac{\bar{Y}}{\bar{X}}$$

where y is the actual net close utilization volume

x is the estimate of close utilization volume

2. Calculate the square of the error of each observation

$$e_i^2 = (y_i - (R * x_i))^2$$

3. For a range of values from -1 to 4 at increments of .001, known as P values, perform the following calculations on each observation:

$ResidualP = (e_i / (x_i)^P)$, and

$Ppvalue = P * log(x_i)$

4. Sum *ResidualP* and *Ppvalues* values for each *P* value.

$= \sum ResidualP \text{ and } \sum Ppvalue$

5. Calculate the average *ResidualP* value for each *P* value.

$Ave\_ ResidualP = ResidualP / No\ of\ trees$

6. Calculate the *LP* value for each *P* value.

$LP = -1 * No\ of\ trees * log(Ave\_ResidualP)$

7. Determine the *P* value that produces the maximum *LP* value. This is the optimum *P* value that is used as the tree weight.

Calculate the Model Sample Tree Weight

Once the optimum *P* value is determined, calculate the sample tree weight, *W*, for trees with an estimate of net close utilization volume > 0 as follows:

$$w_i = (x_i)^{1-p}$$

6.1.4.3 Calculate the NVAF

The NVAF, which is a ratio, is computed using individual tree measurements as follows:

$$R_{tree} = \frac{\textit{weighted average tree volume from destructive sampling}}{\textit{weighted average tree volume from operational measurements}}$$

Substitute in the terms and simplify:

$$NVAF = \frac{\sum_{sample\ trees} w_i * y_i}{\sum_{sample\ trees} w_i * x_i}$$

where y_i is net volume obtained from destructive sampling and

x_i is the estimate of volume obtained from the taper equation and net factoring.

w_i is the sample tree model weight

6.1.4.4 Calculate the NVAF Statistics

Calculate the Variance of the NVAF ratio

The calculation of the NVAF variance occurs through a series of steps

1. Calculate the square of the residual values, which are the difference between actual tree net volume and the product of the computed NVAF and the cruiser-estimated net volume as follows:

   $e_i^2 = (y_i - (NVAF * x_i))^2$

2. Calculate the numerator of the variance equation as:

   $Var\_Num = \sum(e_i^2 * (x_i)^{(2-2*p)})$

3. Calculate the denominator of the variance equation as :

   $Var\_Den = \sum((x_i)^{2-p})$

4. Calculate the variance of the ratio:

   $V(R) = Var\_Num / (Var\_Den)^2$

Calculate the Standard Error of the NVAF Ratio:

The Standard error of the ratio is the square root of the variance of the ratio computed above, and is computed as:

$$SE_R = \sqrt{V(R)}$$

Calculate the Confidence Limits of the NVAF:

1. select the appropriate t value given a level of probability (use 95%), a sample size n and degrees of freedom equal to $n - 2$.
2. confidence limits = NVAF $\pm$ $SE_R * t$

Calculate the Percent Sampling Error:

$SE\% = SE_R * t * 100 / NVAF$

Calculate the Standard Deviation:

$SD = SE_R * \sqrt{n}$

Calculate the Coefficient of Variation:

$CV = 100 * SD / NVAF$

6.2 NVAF Data Compilation – Design Based

6.2.1 Introduction

This section outlines the tasks required to compile tree net merchantable volumes from the destructive stem analysis and VRI ground sample data sets and to calculate the NVAF and its statistics.

The "Design" based method makes use of weights based on the probabilities of the selection of the sample trees.

The Design based method applies to legacy projects only and all projects commenced after 2002 must use the model based calculations.

6.2.2 General Procedures

The general procedures for data compilation and NVAF calculation are outlined sequentially. The detailed procedures follow further in the section.

1. Compilation of the estimates of tree volume
    - Assemble sample information required to run the compiler.
    - Determine appropriate source of the inputs for the taper equation.
    - Compile tree volumes to VRI sample compiler standards
2. Compilation of the actual tree volumes
    - Compile volumes
    - Assess for errors in data
3. Merge the two volume datasets.
4. Calculate the sample tree selection probabilities.
    - Determine ground sample selection weights
    - Calculate sample tree matrix weights.
    - Calculate the prism sweep weight.
    - Calculate overall sample tree weight.
5. Calculate the NVAF
6. Calculate the NVAF statistics.

6.2.3 Detailed Procedures

6.2.3.1 Compilation of the Estimates of Tree Volume

The current standard is the use of the SAS based VRI sample compiler to determine tree volume. The VRI sample compiler utilizes the BEC based taper equations, a facility to deal with broken tops and uses net factoring to estimate decay and waste losses.

Assemble Sample Information Required to Run the Compiler.

The essential sample attributes not found on the VRI raw data file are the administrative unit and biogeoclimatic zonation. These attributes are required as inputs for the BEC based taper equation.

Determine Appropriate Source of the Inputs for the Taper Equation.

The primary inputs for the taper equation are species, dbh and height and there are two sources for this information: the cruiser estimates and the destructive sample. The standard requires the use of the felled dbh and height as inputs for the estimation of gross and close utilization volumes.

Compile Tree Volumes to VRI Sample Compiler Standards

Use the SAS based VRI sample compiler to compile tree volumes or a similar compiler that complies with the VRI compilation standards.

6.2.3.2 Compilation of the Actual Tree Volumes

The current standard is the use of the MSRM TIB (SAS based) volume and decay tree compiler. This compiler uses the DVHand data files as input and produces a standard set of output files.

Compile Volumes

Use the MSRM TIB volume and decay tree compiler.

Assess for Errors in Data

The volume and decay data collection software, DVHand and Host, produce relatively clean data files but can allow some errors to pass undetected. The errors that are critical to the compilation of wood volume are:

- Section gross wood diameters: identify and confirm diameters that increase with increasing tree height.
- Section decay diameters: identify and confirm diameters that exceed gross section diameters.
- Section decay length: identify and confirm decay lengths in the base of the primary and secondary leaders.
- Broken top height and diameter: confirm that the broken top height and diameter match the penultimate sections height and diameter.
- Upper (Utop) utilization height: confirm that there is a section ending at the Utop inside bark diameter.

The volume and decay tree compiler has a limited facility to identify potential data errors primarily in terms of section diameters that exceed expected limits.

For example, the compiler will produce error messages identifying the section diameters that increase with height or decay diameters that exceed the section diameters.

6.2.3.3 Merge the Two Volume Datasets

Merge the dataset containing the estimates of tree volume produced by the VRI sample compiler with compiled volumes produced by the volume and decay tree compiler. The merge attributes are:

- VRI ground sample number and the region, compartment and sample number of the destructive sample data.
- The plot and tree number of both datasets.

6.2.3.4 Calculate the Sample Tree Selection Probabilities

Calculate the Inclusion Probability Due to the Polygon Level Selection

The NVAF sample polygons are selected using an area weighted scheme where the polygon are selected with probability proportional size with replacement (PPSWR). Polygon size in this case refers to the polygon area, and this probability is computed as:

$$P = n \times \frac{A_i}{A} \qquad (1)$$

where n = number of polygon selected for NVAF sampling;

A_i = area of an individual polygon, and

A = total area of the management unit.

Calculate the Inclusion Probability Due to the Prism Sweep

When a prism is used to select NVAF trees in the 4 VRI cluster plots, the probability of a tree to be included in a prism sweep of a ground sample is

$$S = \frac{BA_{ij}}{BAF_i \times A_i} \qquad (2)$$

where $BAij$ is the basal area of the tree,

$BAFi$ is the basal area factor of the sample and

Ai is the area of the polygon.

Since an NVAF tree could come from any of the auxiliary plots, the overall probability that a tree from a particular polygon would be included in the sample due to at least one of the prism sampling points is,

$B = 1-(1-S)^{s_i}$,where si is the number auxiliary plots at a VRI sample location.

For small S values (less than 0.1), $B \approx s_i \times S = s_i \times \frac{BA_{ij}}{BAF_i \times A_i}$ (3)

Calculate the Inclusion Probability Due to a Fixed Area Plot

When a fixed area plot is used to select NVAF trees in the VRI cluster plots, the probability of a tree to be included in the plot is

$$P = s_i * a_i \quad (2)$$

where s_i is the number of auxiliary plots in the sample,

a_i is the area of the plot.

Calculate the Inclusion Probability Due to the Sample Selection Matrix

The probability of selecting a tree from a group *k* is calculated as the ratio of the number of stem analysis trees to the total number of trees enhanced in the selected plots of the VRI NVAF sample clusters, as follows:

$$M = \frac{t_k}{T_k}. \quad (4)$$

where *t* equals the number of stem analysis trees sampled from the group and *T* is the number of trees tallied in the group *k* during the first phase of NVAF data collection.

Calculate the Overall Sample Tree Weight

The overall inclusion probability is the product of the 3 separate inclusion probabilities described above. Hence, the probability that tree *j* of species *k* in polygon *i* will be selected for NVAF sampling is:

π_{ijk} = prob(polygon$_i$) × prob(tree$_j$ in polygon$_i$) × prob(tree$_j$ of species group *k*)

$$\pi_{ijk} = P \times B \times M = n \times \frac{A_i}{A} \times s_i \times \frac{BA_{ij}}{BAF_i \times A_i} \times \frac{t_k}{T_k} = \frac{n}{A} \times \frac{s_i \times BA_{ij}}{BAF_i} \times \frac{t_k}{T_k} \quad (5)$$

where n is the number of polygons chosen for NVAF sampling;

A is the total area of the management area;

s_i is the number prism sweeps in polygon i;

BA_{ij} is the basal area of tree j in polygon i;

BAF_i is the basal area factor used in polygon i;

t_k is the number of trees selected from species group k; and

T_k is the number of trees in species group k.

The overall sample tree weight is the inverse of the quantity π_{ijk}, i.e., the inverse of the probability of selecting a tree.

6.2.3.5 Calculate the NVAF

The NVAF, which is a ratio, is computed using individual tree measurements as follows:

$$R_{tree} = \frac{\textit{weighted average tree volume from destructive sampling}}{\textit{weighted average tree volume from operational measurements}}$$

where the weights are the reciprocal of the overall inclusion probabilities. Substitute in the terms and simplify:

$$NVAF = \frac{\sum_{sample\ trees} \frac{BAF_a}{s_a \times BA_a} \times \frac{T_a}{t_a} \times Y_a}{\sum_{sample\ trees} \frac{BAF_a}{s_a \times BA_a} \times \frac{T_a}{t_a} \times X_a} \qquad (6)$$

where Y_a is net volume obtained from destructive sampling and

X_a is the estimate of volume obtained from the taper equation and net factoring.

This equation (6) is a simplification of Equation (5), in that some common factors in the denominator and numerator are eliminated.

Note that if a fixed area plot has been used to tally trees, the expression $BAF / s_i * BA_{ij}$ is replaced with $1 / s_i * a_i$

6.2.3.6 Calculate the NVAF Statistics

Calculate the Variance of the NVAF ratio

The calculation of the NVAF variance occurs through several steps

Step 1: Calculate the residual values, which are the difference between actual tree net volume and the product of the computed NVAF and the cruiser-estimated net volume as follows:

$$e_i = y_i - (NVAF * x_i) \qquad (7)$$

Step 2: Calculate the variance of the ratio predicted values:

$$V(\hat{Y}_R) = (1-\pi_i)(w_i e_i)^2 \qquad (8)$$

where $V(\hat{Y}_R)$ is the variance of the ratio predicted values

π_i is the total probability of selection for the sample tree

wi is the reciprocal of the π_i value

Step 3: Calculate the variance of the NVAF ratio:

$$V(R) = \frac{\sum V(\hat{Y}_R)}{\bar{x}_w{}^2 \left(\sum w_i\right)^2}, where: -\bar{x}_w = \frac{\sum w_i x_i}{\sum w_i} \qquad (9)$$

Calculate the Standard Error of the NVAF Ratio:

The Standard error of the ratio is the square root of the variance of the ratio computed above, and is computed as:

$$SE_R = \sqrt{V(R)} \qquad (10)$$

Calculate the Confidence Limits of the NVAF:

1. select the appropriate t value given a level of probability (use 95%), a sample size *n* and degrees of freedom equal to $n - 2$.
2. confidence limits = NVAF ± SE_R* t *(11)*

Calculate the Percent Sampling Error:

$SE\% = SE_R * t * 100 / NVAF$ *(12)*

Calculate the Standard Deviation:

$SD = SE_R * \sqrt{n}$ (13)

Calculate the Coefficient of Variation:

$CV = 100 * SD / NVAF$ *(14)*

7.0 Data Analysis Considerations

7.1 Introduction

This section outlines the post project analyses that can lead to a greater understanding of the sources of error in the volume estimates, the need for additional stratification and to assess the need to conduct additional sampling for NVAF.

7.2 General Procedures

The general procedures for post project analyses are outlined. The detailed procedures follow further in the section.

1. Post stratification of sample tree results.
2. Calculation of the taper equation error.
3. Calculation of the errors in loss estimation.
4. Assess the need for additional strata and sample trees.

7.3 Detailed Procedures

7.3.1 Post Stratification of Sample Tree Results

Since most NVAF sampling projects often involve small samples and broad strata that are typically composed of a multitude of species that cover a large and diverse area, post stratification is not recommended and should be used only for exceptional circumstances.

7.3.2 Stratification Criteria

Stratify the sample trees by species, age group and BEC zone. Stratification criteria should be kept at a high level due to the generally small sample sizes.

If the intent is to assess the NVAF to be applied to VRI ground samples, then use criteria that could be applied at the sample level in the VRI plot compiler. Such criteria are any that can be used to group and stratify VRI ground samples such as age, BEC unit or stand conditions. Due to the application method for NVAF in the VRI sample compiler, the only available groupings of trees within a sample is species. Therefore risk group (or something similar) or tree size as measured by dbh or volume represent currently unavailable stratification criteria.

Table 7-1. Example of Variation in NVAF Values by Strata.

Stratum	Sample size	NVAF Value	Sample Error
All live trees	50	1.01	8.5%
Fd	22	.99	6.4%
Pl	17	1.06	12.4%
Cw	5	.91	5.8%

Hw	3	.93	15.6%
At	6	1.21	4.3%
Eastern Pl	7	1.02	15.8%
Western Pl	10	1.1	7.3%

7.3.3 Calculation of the Taper Equation Error

Both the gross whole stem and close utilization volumes can be used to assess errors in the taper equation and both volumes will show differing results. Note that the taper equation is applied to trees that have stem form that can substantially differ from the trees of normal form that were used to fit the equation.

Table 7-2. Example of Taper Error in NVAF Trees

Stratum	Taper Error
All live trees	+2%
Fd	+1%
Pl	+5%
Cw	-2%
Hw	-1%
At	+15%
Eastern Pl	-1%
Western Pl	+9%

7.3.4 Calculation of Loss Estimation Error

The loss estimation error can be calculated through the subtraction of the taper equation error from the NVAF.

Table 7-3. Example of Error in Net Factoring

Stratum	NVAF Value	Taper "NVAF" Value	Net Factor Error
All live trees	1.01	1.02	-1%
Fd	.99	1.01	+2%
Pl	1.06	1.05	-1%
Cw	.91	.98	-7%
Hw	.93	.99	-6%

At	1.21	1.15	+6%
Eastern Pl	1.02	.99	+3%
Western Pl	1.1	1.09	+2%

7.3.5 Identify Outliers or Influence Trees

Influence trees are ones that due to their large volume can have a great affect on the NVAF value. It is possible for a single tree to cause the NVAF and the sample error to vary by as much as 10%. These trees are part of the valid sample and must be remain in the sample but their identification and influence can be used to guide additional sampling and stratification.

Table 7-4. Example of Outlier Tree.

Stratum	Sample size	NVAF Value	Sample Error
Pl	17	1.06	12.4%
Excluding Outlier	16	1.12	5.1%
Outlier Tree	1	.89	

7.3.6 Assess the Need for Additional Strata and Sample Trees

Providing there is a strong business need, the two primary factors that could drive the need for additional NVAF sampling is large sample errors or large differences between NVAF values for common species in a mixed species stratum.

In most cases the NVAF sample is a small sample of 50 to 100 trees that seeks to provide broad level adjustments for several mixed species strata, usually where the stratification criteria is by age group. Given that the NVAF and net factoring methods are relatively new to the province, there is a shortage of existing information that could be used to establish trends in the differences between the estimate and actual volume by species, age or BEC. Analysis of the results is often the only place to determine which species, if any, within the stratum would have differing NVAFs if sampled separately. For species of economic importance, several inventory units have conducted additional sampling in order to substantiate trends shown in the first sample. Since the sample trees have been selected without bias and sampled at a common standard, they can be pooled with the new trees to calculate more refined NVAFs. The sample errors calculated from the initial sampling project can be used to calculate the number of additional sample trees required to obtain the sample error target.

Using the same example the application of the overall NVAF value will result in substantial increase in Cw and Hw volumes and a decrease in Pl and At volumes than if separate species strata values were applied. If this is an unacceptable compromise, additional sampling should be considered in order to stratify by species or species group.

8.0 Data Requirements

8.1 Introduction

This section outlines the TIB data requirements for NVAF in terms of the raw and compiled VRI: ground sample data, raw and compiled destructive sample data, sample tree probabilities of selection, NVAF stratification criteria and NVAF values.

8.2 General Procedures

1. Data sharing requirement
2. Ground sample and sample tree attributes of interest
3. Tracking weights
4. Tracking strata
5. Sample substitution and replacement

8.3 Detailed Procedures

8.3.1 Data Sharing Requirement

Terrestrial Information Branch has two primary uses for the NVAF data: project audits and the provincial volume and decay program. In order to confirm the NVAF calculation and to use the sample tree for future volume and decay purposes, all information pertaining to the selection of the ground samples and sample trees will be required.

8.3.2 Ground Sample and Sample Tree Attributes of Interest

Raw Destructive Sample Tree Data

All eight files produced by the DVH and Host data collection software.

Raw Ground Sample Data

The output text file produced either by the VIDE data entry software or the VRI ground sample data collection software.

Compiled Destructive Sample Tree Data

All of the files produced by the SAS based TIB volume and decay tree compiler. If an alternate compilation process was used, then gross whole stem, gross merchantable and merchantable volume less decay and waste are required.

Compiled Ground Sample Data

All of the compiled data files produced by the SAS based TIB VRI plot compiler. If an alternate compilation process was used, then the estimates of gross whole stem , gross merchantable less decay and waste are required. Tree volume compilation must be based on the appropriate BEC based taper equation and the VRI net factoring process.

8.3.3 Tracking Weights

VRI Ground Sample Plan

The VRI ground sample plan contains information on the population, the NVAF stratification, number, identity and selection criteria for NVAF ground samples and the number and selection criteria of NVAF sample trees.

Sample Tree Weights

All of the sample tree weights for each sample tree must be supplied.

8.3.4 Tracking Strata

VRI Analysis Report

The VRI analysis report cites the strata and their values used in the adjustment of VRI ground samples.

8.3.5 Sample Substitution and Replacement

The reason for changes made to the plan during the implementation of the sample for ground samples and sample trees and the identity of replacement or substituted sample and sample trees must be described.

9.0 Use of NVAF in the Compiler

9.1 Introduction

This section outlines the application of the NVAF in the adjustment of the VRI ground sample volumes. The NVAF is applied at the sample level at the end of the sample compilation process.

9.2 General Procedures

1. Meta data
2. Application

9.3 Detailed Procedures

9.3.1 Meta Data

The common types of meta data for NVAF is information that allows for the stratification of the VRI ground samples or species into groups that require specific NVAF adjustments.

Most VRI projects elect to stratify the NVAF into two age groups based on polygon age (immature and mature) and in addition, the mature strata is stratified into groups based on major species and a combination of all of the minor species.

9.3.2 Application

The NVAF is applied at the sample level and acts as a multiplier of the volume per hectare of the stratum. This application method is equivalent to the adjustment of each tree's net merchantable volume.

Table 9-1. Example of the NVAF Adjustment.

Stratum	Unadjusted ground sample volume per hectare	NVAF adjustment	Adjusted ground sample volume per hectare
Fd	262.9 m3/ha	1.015	266.8 m3/ha
Hw	174.8 m3/ha	.923	161.3 m3/ha
Dr	31.7 m3/ha	.951	30.1 m3/ha
Cw	12.0 m3/ha	.951	11.4 m3/ha
Total	481.4 m3/ha		469.6 m3/ha

10.0 Quality Assurance and Data Collection Standards

10.1 Introduction

This section outlines the quality assurance procedures and the data collection standards for NVAF sampling. The intent of quality assurance (QA) is to determine the overall quality of the NVAF sample. The QA information is used for contractual payment purposes and to identify errors if remedial action is required. Due to the destructive nature of the NVAF sample, it is impossible to consider the QA as an independent sample.

A minimum of 10% of the sample trees must be inspected in order to determine the overall quality of a batch of sample trees. The batch is passed if 90% of the inspected sample trees meet the sampling standards. Use a guideline of one ground sample to be selected for every 30 NVAF sample trees. Therefore a NVAF sample of approximately 60 trees will require a minimum of 6 trees inspected from a minimum of 2 separate VRI ground samples. The standard is to select randomly select ground samples and sample trees for the field inspection. Since NVAF sample trees range in sampling difficulty, stratification by decay or difficulty class and a proportional selection from each class will ensure that range of trees are selected for quality assurance.

The standards for NVAF inventory cruising adhere to the ones set for the VRI ground sample. Refer to the VRI ground sampling standards and procedures document.

Due to the rapid weathering of NVAF sample trees, QA should be done within a few weeks of the sampling.

10.2 General Procedures

1. **Determine the sample sizes for inspection**
   - Stratify the sample trees by difficulty class
   - Identify the ground samples with difficult trees
   - Calculate the sample size for ground samples and sample trees by difficulty class
2. **Select the sample locations and trees.**
   - Select ground samples
   - Select sample trees
   - Select replacement samples and trees
3. **Conduct field inspection.**
4. **Summarize the results and determine overall quality**
   - Calculate the differences between audit and sampler measurements
   - Calculate the penalty points
   - Summarize and report results
   - Determine overall quality
5. **Recommend specific remedial action if necessary.**

10.3 Detailed Procedures:

10.3.1 Determine the Sample size For Inspection

10.3.1.1 Stratify the Sample trees into Difficulty Classes

If the sample trees are grouped into classes that reflect the complexity of NVAF sampling, then 10% of the trees from each class are selected for inspection. Immature trees lacking decay or aberrant form can be considered to be the least difficult; over mature trees with decay and aberrant form would be the most difficult to sample. Usually only two difficulty classes are created for QA purposes. The intent is to ensure that all types of trees are inspected in order to properly assess the overall quality of the sampling.

10.3.1.2 Identify the Ground Samples that Contain Difficult Trees

The ground samples are stratified based on the presence or absence of difficult trees. Use the decay tree reports to identify decayed or difficult trees.

10.3.1.3 Calculate the Sample Size for Ground Samples and Sample Trees

The sample size for inspected trees is based on the target of an inspection of a minimum 10% of the trees in the batch. The sample size for ground samples is determined by using a guideline of one ground sample for every 30 sample trees. For example, if the batch consists of 40 trees, then select 2 ground samples and 4 sample trees.

If the sample trees are stratified into two difficulty classes then select 10% of the sample trees from each class. Increase the stratum sample size in order to ensure that the combined selection amounts to at least 10% of the overall batch. To ensure that difficult trees are selected, select a ground sample from the batch of samples that contain difficult trees.

10.3.2 Select Sample Locations and Trees

10.3.2.1 Select Ground Samples

Assign a random number to each ground sample, sort by random number and select from the top of the list.

10.3.2.2 Select Sample Trees

Assign a random number to each sample tree, sort by random number and select from the top of the list.

10.3.2.3 Select Replacement Samples and Trees

Logistical problems may prevent an inspection of the selected sample and mechanical problems, such as the selected tree may be irretrievably buried under other sample trees that may prevent the inspection of the selected tree, consequently replacement samples and trees should be selected in advance.

If a sample tree cannot be inspected, select the next tree from the sorted list.

If a ground sample cannot be inspected, select the next sample from the sorted list and the first tree from the sorted list of trees within the sample.

10.3.3 Conduct the Field Inspection

There are two processes to inspect: the sample tree measurements and the procedures used to measure the tree. Since this is not an independent measure, the inspector's role is to determine the adequacy of the samplers measurement and their application of due diligence. The inspector must carry a copy of the sampler's measurements on site and refer to them at each measurement. In order to produce an actual net merchantable volume for the sample tree, the allowable errors around each measure are relatively tight. However, the destructive nature of the sampling or the often incipient nature of decay can create situations where it is impossible for the inspector to measure precisely. Therefore the inspector must make a decision in the field about the quality of the measure and the sampler's adherence to due diligence. The 'benefit of the doubt' rule must be used. Since inspectors do not carry chain saws, the inspector can only work with the existing condition of the tree and cannot cut new sections or cookies. The inspector should double check all measurements that appear to deviate from the standard.

All tree attributes are inspected.

10.3.4 Summarize Results and Determine Overall Quality

10.3.4.1 Calculate the Differences Between Auditor and Sampler Measurements

Calculate the differences between the two sets of measurements in absolute terms and percentages. Use an elliptical formula to calculate the cross sectional area of a section or a decay.

When an absolute standard and a percentage standard are both cited, then the standard that allows the greater tolerance is used. For example, if the dbh is found to be 34.8 cm and the contractor measure is 34.6, the absolute difference is 0.2 cm and the percentage difference is 0.57%. In this case, the absolute difference is used and the measure conforms to standard.

10.3.4.2 Calculate Penalty Points

Penalty points are assigned when a measure fails to comply to the standards. The type and magnitude of the error determines the number of penalty points.

Section decay diameters in the interpolated butt section are based on the 0.3 and 1.3 meter sections and should not penalized if the basis for the decay interpolation is in error.

If decay has been missed in a section or has been measured where it does not exist, assess penalty points on the basis of decay area, not on decay length. If the intermediate bucking in a section is done incorrectly, then assign the double amount of penalty points for this error.

The penalty for missing or miscalling path indicators is based on allowing 1 poor call for every 5 instances of the specific path indicator. For instance if 6 scars were recorded for the tree and only 5 were found, there would not be a penalty. However, if only 4 were found, then there would be a penalty.

Points are assigned when the measure fails to comply to the standards (Table 7). The magnitude of the error determines the number of points. For instance, if a contractor has recorded 95 years for a 100 year old tree, two points are assigned. If the contractor had recorded 91 years, then 4 points are assigned.

Table 10-1. Standards and Penalty Points for NVAF volume and decay sampling.

Sampling attribute	Sampling standards for individual measure	Audit points if beyond standard	
		< 2 X	≥ 2 X
Sample tree not sampled	No error permitted if capable of being sampled	10	
Sample tree not correctly identified	No error permitted	10	
Sample tree cookies not cut and properly identified	No error permitted	10	
Sample tree not correctly identified	No error permitted	10	
Butt taper heights per measure	± 5 cm	2	4
Butt taper diameters outside bark @ 0.3, 0.6, 0.9, and 1.3 m heights per measure	± 0.2 cm or 0.5%	2	4
Butt taper double bark thickness per measure	± 0.3 cm or 6%	1	2
Age, countable portion	± 2 yr or 4%	2	4
Age, countable and uncountable portion lengths	± 1 cm per measure	1	2
Age, counted height	± 10 cm	1	2
Age correction	± 3 yrs	1	2
Species	No error permitted	10	
Total tree length, if intact	± 10 cm	4	8
Total tree length, if broken by felling	± 25 cm	4	8
Estimated length of section above a broken top	± 2 m	4	8
Primary upper utilization point height	± 10 cm	4	8
Secondary leader length, if intact	± 20 cm	2	4
Secondary leader length, if broken by felling	± 40 cm	2	4
Secondary upper utilization point height	± 15 cm	2	4
Secondary leader starting heights, upper and lower locations	± 10 cm per measure	2	4
Section upper and lower locations	± 10 cm	1	2
Section length	± 5 cm	2	4
Section cross-sectional area, if has a regular circumference.	± 8 cm^2 or 2%	2	4
Section cross-sectional area, if collapsed or has a very irregular circumference	± 20 cm^2 or 4%	2	4
Loss indicators standing or felled, number by type *	± 80%	4	
Loss indicator lower and upper locations	± 10 cm per measure	1	2
Loss indicator scar width	± 2 cm or 20%	0.5	1
Section decay length *	± 25 cm	1	2
Section decay cross sectional area, if intact	± 10 cm^2 or 5%	2	4

Sampling attribute	Sampling standards for individual measure	Audit points if beyond standard	
		< 2 X	≥ 2 X
Section decay cross sectional area, if collapsed *	± 20 cm^2 or 10%	2	4
Hidden decay investigation per path indicator	no error permitted	5	
Decay type	± 1 class	0.5	
Section decay percentage for mixed decays	± 10%	0.5	1
Crown height	± 1 m	0.5	1
Biogeoclimatic zonation	no error	5	
Site series	± 1 series	1	2
Slope position	± 1 position	1	2
Slope percent	± 10%	1	2
Aspect	± 20°	1	2
Elevation	± 100 m	1	2

* Denotes a more detailed explanation in 'Calculate Penalty Points' section that precedes the Standards Table.

10.3.4.3 Summarize and Report Results

Summarize the results of the inspection in terms of:

- The type, magnitude and penalty points of each error for each sample tree.
- Total penalty points for each tree.
- The ratio of the number of trees that pass the inspection over the total number of trees inspected.

10.3.4.4 Determine Overall Quality

Report the end result of the inspection in terms of pass or failure.

An example of an inspection report is contained in Figure 10-1 below.

2002 Bobs Lk NVAF Sample QA Inspection
Auditor: Will Smith Audit Dates: Sept 16,17& Oct 2,3 2002

Overall Result of QA Inspection	Pass

Audit Results:

Number of Trees Audited:	9
Number of Trees Meeting the Standard	9
Percentage of Trees Meeting the Standard	100%

Audit Summary per Tree

Sample	Tree #	Penalty Pts	Pass/Fail
57	N-2	0	Pass
171	N-2	2	Pass
171	W-1	6	Pass
171	W-3	0	Pass
174	E-2	6	Pass
174	N-5	2	Pass
194	N-5	2	Pass
195	E-2	4	Pass
195	E-5	0	Pass

Summary of Errors

			Measures		Difference		Penalty
Sample	Tree #	Attribute	Inspector	NVAF Sampler	Absolute	%age	Points
171	N-2	.3 section Decay	6	9	- 2.3	-35.3%	0
171	N-2	conk path	0	1	- 1.0	100.0%	4
171	W-1	2.3 section area	177	170	7.2	4.1%	0
171	W-1	Counted Age	165	154	11.0	6.7%	2
174	E-2	Counted Age	160	145	15.0	9.4%	4
174	E-2	10.3 section area	244	252	- 8.2	-3.4%	2
174	E-2	14.3 section area	155	159	- 4.5	-2.9%	0
174	N-5	Counted Age	225	234	- 9.0	-4.0%	0
174	N-5	Scar path	1	0	1.0	100.0%	4
194	N-5	10.3 section area	305	299	6.2	2.0%	0
194	N-5	14.3 section area	190	181	8.4	4.4%	2
195	E-2	Frost crack path	0	3	- 3.0	300.0%	4
195	E-5	Scar path	9	8	1.0	88.9%	0
195	E-5	2.3 section area	635	629	6.2	1.0%	0

Figure 10-1. Example of QA Inspection Report.

10.3.5 Recommend specific remedial action if necessary

If the inspection has found the work to fail to meet the standard, then some sort of remedial action will be required in order to use the data for its intended purpose. If at all possible, the inspector should identify specific types of errors that require correction in order to provide a focus to the remedial action.

10.3.6 Send a Copy of the Audit Report to MSRM

Send a copy of the field inspection to Will Smith at RIB.

11 Definitions

The following acronyms and terms may be encountered in this manual. Their meaning is provided here to facilitate easy reference, and make it easier to follow the description of the procedures.

NVAF: Net volume adjustment factor is a factor used to adjust net tree volumes estimated from net factoring and taper equations. The NVAF adjustment accounts for errors in loss estimation (decay and waste) and possible taper equation bias.

VRI: Vegetation Resources Inventory is a toolbox of inventory procedures for assessing the quantity and quality of BC's vegetation resources that includes: BC Landcover Classification Scheme (BCLCS), Phase I, Phase II, NVAF Sampling, Within Polygon Variation sampling (WPV) sampling, and Change Monitoring Inventory (CMI).

RIB: Research Information Branch of the Ministry of Sustainable Resource Management

MSRM: Ministry of Sustainable Resource Management

MOF: Ministry of Forests

ROM: Ratio of means

PPSW: Probability proportional to size with replacement

Net Factoring: The process of estimating a "net factor", which is an estimate of the % sound wood (less decay) in each log of the tree.

Stem Analysis: The felling, sectioning and measuring of tree sections to estimate volume or study other tree characteristics, otherwise known as destructive sampling for volume and decay.

Cruiser Estimated Net Volume: Net close utilization tree volume obtained by adjusting the gross volume from taper equations to account for decay and waste loss determined by the net factoring process

Actual Net Volume: Close utilization tree volume obtained by summing the sound wood volumes (less decay and waste) of sections of a stem analysed tree.

Weights: Multipliers needed to account for variable sample selection probabilities.

Population: The entire collection of the elements of interest. In the NVAF, the population is typically all trees with a dbh equal to or greater than 12.5cm in an inventory unit, such as a TFL or TSA.

Sampling Frame: A collection of information describing the members or elements of the population. The information should include a complete list of the sampling unit.

maps or notes identifying where the individual sampling units are located and attributes defining the characteristics of the sampling units.

Sampling Unit: Is the smallest indivisible component of a population, which is listed in a sampling frame and is eligible for selection to form a sample. In NVAF sample selection, the sampling frame consists of trees of different species, therefore the NVAF sampling unit is a tree.

Sub-population: A higher-level division of the population; it maybe a specific geographic area or stand type within the population.

Stratum: A sub-division of the population or sub-population (e.g., by leading tree species).